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OM protein - protein search, using sw model

Run on: August 3, 2004, 09:08:27 ; Search time 19 Seconds
(without alignments)
1130.337 Million cell updates/sec

Title: US-09-961-201A-1

Perfect score: 416

Sequence: 1 MDEADRLRLRRCLRLVEEL.....YKQPGCFNLRKLFKTS 416

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/2/iaa/5A COMB.pep.*
- 2: /cgn2_6/prodata/2/iaa/5B COMB.pep.*
- 3: /cgn2_6/prodata/2/iaa/6A COMB.pep.*
- 4: /cgn2_6/prodata/2/iaa/6B COMB.pep.*
- 5: /cgn2_6/prodata/2/iaa/PCFUS COMB.pep.*
- 6: /cgn2_6/prodata/2/iaa/backfilees1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	416	100.0	416	3	US-08-852-936C-1
2	416	100.0	416	3	US-09-300-328-1
3	416	100.0	416	4	US-09-069-023-23
4	219	52.6	416	4	US-09-561-756-30
5	219	52.6	416	4	US-09-227-721-30
6	219	52.6	416	4	US-09-954-697-30
7	202	48.6	203	3	US-08-852-936C-4
8	202	48.6	203	3	US-09-300-328-4
9	195	46.9	416	3	US-09-257-218-2
10	195	46.9	416	3	US-09-311-760-2
11	195	46.9	416	4	US-08-865-579-2
12	195	46.9	416	4	US-10-059-749-2
13	15	3.6	15	3	US-09-257-218-22
14	15	3.6	15	3	US-09-311-760-22
15	15	3.6	15	4	US-09-561-756-59
16	15	3.6	15	4	US-09-227-721-59
17	15	3.6	15	4	US-08-865-579-22
18	15	3.6	15	4	US-10-059-749-22
19	15	3.6	15	4	US-09-954-697-59
20	15	3.6	46	3	US-09-257-218-6
21	15	3.6	46	3	US-09-311-760-6
22	15	3.6	46	4	US-08-865-579-6
23	15	3.6	46	4	US-10-059-749-6
24	11	2.4	299	2	US-08-773-688A-2
25	10	2.4	39	4	US-09-187-789-38
26	10	2.4	39	4	US-09-139-600-33
27	10	2.4	303	3	US-08-462-969B-2

28	10	2.4	303	4	US-09-561-756-24	Sequence 24, Appl
29	10	2.4	303	4	US-09-227-721-24	Sequence 24, Appl
30	10	2.4	303	4	US-08-556-627A-2	Sequence 2, Appl
31	10	2.4	303	4	US-09-124-934A-2	Sequence 2, Appl
32	10	2.4	303	4	US-08-724-378D-4	Sequence 4, Appl
33	10	2.4	303	4	US-08-334-251D-2	Sequence 2, Appl
34	10	2.4	303	4	US-09-954-697-24	Sequence 24, Appl
35	10	2.4	303	4	US-09-163-099-2	Sequence 2, Appl
36	10	2.4	346	2	US-08-618-408B-2	Sequence 2, Appl
37	10	2.4	389	4	US-08-724-378D-2	Sequence 2, Appl
38	10	2.4	389	4	US-08-665-220-2	Sequence 3, Appl
39	10	2.4	479	1	US-09-291-692-2	Sequence 2, Appl
40	10	2.4	479	3	US-09-561-756-33	Sequence 33, Appl
41	10	2.4	479	4	US-09-227-721-33	Sequence 4, Appl
42	10	2.4	479	4	US-09-954-697-33	Sequence 4, Appl
43	10	2.4	479	4	US-09-009-893A-4	Sequence 2, Appl
44	10	2.4	479	4	US-09-962-834A-2	Sequence 4, Appl
45	10	2.4	521	4	US-09-489-155-4	Sequence 2, Appl
46	10	2.4	521	4	US-09-311-760-19	Sequence 19, Appl
47	9	2.2	9	3	US-09-257-218-19	Sequence 19, Appl
48	9	2.2	9	3	US-09-311-760-19	Sequence 19, Appl
49	9	2.2	9	4	US-09-561-756-56	Sequence 56, Appl
50	9	2.2	9	4	US-09-227-721-56	Sequence 56, Appl
51	9	2.2	9	4	US-08-865-579-19	Sequence 19, Appl
52	9	2.2	9	4	US-10-059-749-19	Sequence 19, Appl
53	9	2.2	9	4	US-09-954-697-56	Sequence 56, Appl
54	9	2.2	1196	3	US-08-881-706-2	Sequence 2, Appl
55	8	1.9	141	4	US-09-252-991A-16951	Sequence 16951, A
56	8	1.9	1218	4	US-09-198-452A-98	Sequence 98, Appl
57	7	1.7	25	4	US-09-257-179-96	Sequence 96, Appl
58	7	1.7	141	4	US-09-252-991A-25224	Sequence 25224, A
59	7	1.7	150	4	US-09-198-452A-1023	Sequence 1023, Ap
60	7	1.7	202	4	US-09-257-179-90	Sequence 90, Appl
61	7	1.7	248	4	US-09-252-991A-29249	Sequence 29249, A
62	7	1.7	253	4	US-09-252-991A-22878	Sequence 22878, A
63	7	1.7	304	4	US-09-252-991A-23222	Sequence 23222, A
64	7	1.7	313	4	US-09-252-991A-30181	Sequence 30181, A
65	7	1.7	318	4	US-09-292-858B-24	Sequence 24, Appl
66	7	1.7	324	4	US-09-328-352-6612	Sequence 6612, Ap
67	7	1.7	339	4	US-09-252-991A-27733	Sequence 27733, A
68	7	1.7	358	4	US-09-489-039A-9326	Sequence 9326, Ap
69	7	1.7	369	4	US-09-252-991A-23356	Sequence 23356, A
70	7	1.7	373	4	US-09-489-039A-11774	Sequence 11774, A
71	7	1.7	401	1	US-08-198-446B-11	Sequence 11, Appl
72	7	1.7	401	2	US-08-870-693-11	Sequence 11, Appl
73	7	1.7	419	4	US-09-134-001C-3441	Sequence 3441, Ap
74	7	1.7	423	4	US-09-328-352-6273	Sequence 6273, Ap
75	7	1.7	426	4	US-09-252-991A-29288	Sequence 29288, A

ALIGNMENTS

RESULT 1

US-08-852-936C-1
; Sequence 1, Application US/08852936C
; Patent No. 6010878

GENERAL INFORMATION:

APPLICANT: DIXIT, VISHVA M.
APPLICANT: HE, WEI-WU
APPLICANT: KIKLY, KRISTINE K.
APPLICANT: RUBEN, STEVEN M.
TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:

APPLICANT: RUBEN, STEVEN M.
 TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
 TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ratner & Prestia
 STREET: P.O. Box 980
 CITY: Valley Forge
 STATE: PA
 COUNTRY: USA
 ZIP: 19482
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/300,328
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/852,936
 FILING DATE: 08-MAY-1997
 APPLICATION NUMBER: 60/018,961
 FILING DATE: 05-JUN-1996
 APPLICATION NUMBER: 60/020,344
 FILING DATE: 23-MAY-1996
 APPLICATION NUMBER: 60/017,949
 FILING DATE: 20-MAY-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Prestia, Paul F
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: P50483-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0700
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 416 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-300-328-1

Query Match	100.0%;	Score 416;	DB 3;	Length 416;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 416;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1	MDEADRLRRCLRRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII	60		
1	MDEADRLRRCLRRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII	60		
61	DLETRGSQALPFTISCLDTEQDQMLASFRLTNROAGKLSKPTLENLTPVVLPEIRPEV	120		
61	DLETRGSQALPFTISCLDTEQDQMLASFRLTNROAGKLSKPTLENLTPVVLPEIRPEV	120		
121	LRPPTPRVDITGSGFGDVGALESLRGNADLAYILSMGPCGHCLIIINNVPFCRESGLRTR	180		
121	LRPPTPRVDITGSGFGDVGALESLRGNADLAYILSMGPCGHCLIIINNVPFCRESGLRTR	180		
181	TGSNIDCEKLRRRRFSSLFHFVVEVKGDLTAKKMWLALLELARQDGHGALDCCVWVILSHGQC	240		
181	TGSNIDCEKLRRRRFSSLFHFVVEVKGDLTAKKMWLALLELARQDGHGALDCCVWVILSHGQC	240		
241	ASHLQFPGAVGTDCQPSVSEKIVNI FNGTSCPSLGGKPKLFFFTQACGGEQKDGHFEVAS	300		
241	ASHLQFPGAVGTDCQPSVSEKIVNI FNGTSCPSLGGKPKLFFFTQACGGEQKDGHFEVAS	300		
301	TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLTPSDIFVSYSTTFPGVSWDRDPKSG	360		
301	TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLTPSDIFVSYSTTFPGVSWDRDPKSG	360		
361	SNYVETLDDIFQWHAHSEDQLSLLLRVANAVSVKGIYQMPCCFNFLRKLFFKTS	416		
361	SNYVETLDDIFQWHAHSEDQLSLLLRVANAVSVKGIYQMPCCFNFLRKLFFKTS	416		

RESULT 2
US-09-300-328-1
; Sequence 1, Application US/09300328
; Patent No. 6294169
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.

QY 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
 Db 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

RESULT 3

US-09-069-023-23
 ; Sequence 30, Application US/09069023A
 ; Patent No. 6348573

GENERAL INFORMATION

APPLICANT: Nunez, Gabriel
 APPLICANT: Inohara, Naohiro
 APPLICANT: Koseki, Takeyoshi
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
 TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
 FILE REFERENCE: UM-0333
 CURRENT APPLICATION NUMBER: US/09/069,023A
 CURRENT FILING DATE: 1998-04-27
 NUMBER OF SEQ ID NOS: 38
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 23
 LENGTH: 416
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-069-023-23

Query Match 100.0%; Score 416; DB 4; Length 416;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVLDVLLSRELFRPHMETIQAGSGRRDQARLII 60
 Db 1 MDEADRLRLRCRLRLVEELQVLDVLLSRELFRPHMETIQAGSGRRDQARLII 60
 QY 61 DLETRGQALPLFISCLEDTGQDLASFLTNQAGKLSKPTLENLTPVLRPEIRKPEV 120
 Db 61 DLETRGQALPLFISCLEDTGQDLASFLTNQAGKLSKPTLENLTPVLRPEIRKPEV 120
 QY 121 LRPETPRPVDIGSGGFDVGALESRLGNADLAVILSMPECGHCLIIINNVCRESGLRTR 180
 Db 121 LRPETPRPVDIGSGGFDVGALESRLGNADLAVILSMPECGHCLIIINNVCRESGLRTR 180
 QY 181 TGSNIDCEKLRFRFSSLHFMEVVKGLTAKKMWLALLELARQDHGALDCCVVILSHGCO 240
 Db 181 TGSNIDCEKLRFRFSSLHFMEVVKGLTAKKMWLALLELARQDHGALDCCVVILSHGCO 240
 QY 241 ASHLQPPGAVYCTDGCPSVSEKIUNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300
 Db 241 ASHLQPPGAVYCTDGCPSVSEKIUNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300
 QY 301 TSPDESPGSGNPEPDATPFQEGRLTFDQDLDAISSLPTPSDIFVSYSTFPFGFVSWRDPKSG 360
 Db 301 TSPDESPGSGNPEPDATPFQEGRLTFDQDLDAISSLPTPSDIFVSYSTFPFGFVSWRDPKSG 360
 QY 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
 Db 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

RESULT 4

US-09-561-756-30
 ; Sequence 30, Application US/09561756
 ; Patent No. 6376226

GENERAL INFORMATION

APPLICANT: Alnemri, Emad S.
 TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
 TITLE OF INVENTION: THEREOF
 FILE REFERENCE: 480140.431
 CURRENT APPLICATION NUMBER: US/09/561,756
 CURRENT FILING DATE: 2000-04-26
 PRIOR APPLICATION NUMBER: 09/227,721
 PRIOR FILING DATE: 1999-01-08

; NUMBER OF SEQ ID NOS: 116
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 30
 ; LENGTH: 416
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-561-756-30

Query Match 52.6%; Score 219; DB 4; Length 416;
 Best Local Similarity 100.0%; Pred. No. 8.1e-203;
 Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 HFMEVVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCOASHLOFPFGAVYGTDCGP 257
 Db 198 HFMEVVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCOASHLOFPFGAVYGTDCGP 257
 QY 258 VSVEKIUNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPESPGSNPEPDAT 317
 Db 258 VSVEKIUNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPESPGSNPEPDAT 317
 QY 318 PFQEGRLTFDQDLDAISSLPTPSDIFVSYSTFPFGFVSWRDPKSGWYVETLDDIFEQWAHS 377
 Db 318 PFQEGRLTFDQDLDAISSLPTPSDIFVSYSTFPFGFVSWRDPKSGWYVETLDDIFEQWAHS 377
 QY 378 EDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
 Db 378 EDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

RESULT 5

US-09-227-721-30
 ; Sequence 30, Application US/09227721
 ; Patent No. 6379950

GENERAL INFORMATION

APPLICANT: Alnemri, Emad S.
 TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
 TITLE OF INVENTION: THEREOF
 FILE REFERENCE: 480140.431
 CURRENT APPLICATION NUMBER: US/09/227,721
 CURRENT FILING DATE: 1999-01-08
 NUMBER OF SEQ ID NOS: 116
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 30
 LENGTH: 416
 TYPE: PRT
 ORGANISM: Homo sapien
 US-09-227-721-30

Query Match 52.6%; Score 219; DB 4; Length 416;
 Best Local Similarity 100.0%; Pred. No. 8.1e-203;
 Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 HFMEVVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCOASHLOFPFGAVYGTDCGP 257
 Db 198 HFMEVVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCOASHLOFPFGAVYGTDCGP 257
 QY 258 VSVEKIUNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPESPGSNPEPDAT 317
 Db 258 VSVEKIUNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPESPGSNPEPDAT 317
 QY 318 PFQEGRLTFDQDLDAISSLPTPSDIFVSYSTFPFGFVSWRDPKSGWYVETLDDIFEQWAHS 377
 Db 318 PFQEGRLTFDQDLDAISSLPTPSDIFVSYSTFPFGFVSWRDPKSGWYVETLDDIFEQWAHS 377
 QY 378 EDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
 Db 378 EDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

RESULT 6

US-09-954-697-30
 ; Sequence 30, Application US/09954697
 ; Patent No. 6610541

us-09-961-201a-1.oligo.ra1

Tue Aug 3 09:36:12 2004

REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: p50483-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-852-936C-4

Query Match 48.6%; Score 202; DB 3; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.1e-186; Gaps 0;
Matches 202; Conservative 0; Mismatches 0; Indels 0;

QY 212 MVLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTGCPVSVKIVNIFNGTS 271
Db 1 MVLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTGCPVSVKIVNIFNGTS 60
QY 272 CPSLGGKPKLFFIOACGGEQKDHGFVASTSPEDSPGSPNPEPDATPQGLRTFDQDA 331
Db 61 CPSLGGKPKLFFIOACGGEQKDHGFVASTSPEDSPGSPNPEPDATPQGLRTFDQDA 120
QY 332 ISSLPTSDIFVSYSTPFGVSWDRPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAV 391
Db 121 ISSLPTSDIFVSYSTPFGVSWDRPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAV 180
QY 392 SVKGIYKQMPGCFNLRKLLFF 413
Db 181 SVKGIYKQMPGCFNLRKLLFF 202

RESULT 8

US-09-300-328-4
Sequence 4, Application US/09300328
Patent No. 6294169
GENERAL INFORMATION:
APPLICANT: DIXIT, VISHVA M.
APPLICANT: HE, WEI-WU
APPLICANT: KIKLY, KRISTINE K.
APPLICANT: RUBEN, STEVEN M.
TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/300,328
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/852,936
FILING DATE: 08-MAY-1997
APPLICATION NUMBER: 60/018,961
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: 60/020,344
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: 60/017,949
FILING DATE: 20-MAY-1996

GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
FILE REFERENCE: 480140.431D2
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 30
LENGTH: 416
TYPE: PRT
ORGANISM: Homo sapien
US-09-954-697-30

Query Match 52.6%; Score 219; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 8.1e-203; Indels 0;
Matches 219; Conservative 0; Mismatches 0; Gaps 0;

QY 198 HFVVEVKGDLTAKMVLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTGCP 257
Db 198 HFVVEVKGDLTAKMVLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTGCP 257
QY 258 VSVKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFVASTSPEDSPGSPNPEPDAT 317
Db 258 VSVKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFVASTSPEDSPGSPNPEPDAT 317
QY 318 PQGLRTFDQDAISSLPTSDIFVSYSTPFGVSWDRPKSGSWYVETLDDIFEQWAHS 377
Db 318 PQGLRTFDQDAISSLPTSDIFVSYSTPFGVSWDRPKSGSWYVETLDDIFEQWAHS 377
QY 378 EDLSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
Db 378 EDLSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 7

US-08-852-936C-4
Sequence 4, Application US/08852936C
Patent No. 6010878
GENERAL INFORMATION:
APPLICANT: DIXIT, VISHVA M.
APPLICANT: HE, WEI-WU
APPLICANT: KIKLY, KRISTINE K.
APPLICANT: RUBEN, STEVEN M.
TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,936C
FILING DATE: 08-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/018,961
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: 60/020,344
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: 60/017,949
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F


```

; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-257-218-2

Query Match          46.9%; Score 195; DB 3; Length 416;
Best Local Similarity 100.0%; Pred. NO. 1.1e-179;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      222 QDHGALDCCVVVILSHGCQASHIQFGAVYGTGDCPVSVSEKIVNFNGTSCPSLGGKPKL 281
Db      222 QDHGALDCCVVVILSHGCQASHIQFGAVYGTGDCPVSVSEKIVNFNGTSCPSLGGKPKL 281

QY      282 FFIQACGGEOKDHGFVASTSPEDSPGNSPEPDATPFQEGLRFTFDQLDAISSLPTFSDI 341
Db      282 FFIQACGGEQKHGFVASTSPEDSPGNSPEPDATPFQEGLRFTFDQLDAISSLPTFSDI 341

QY      342 FVSYSTFPFVSWRDPKSGSWYVETLDDIFEQWAGHSEDLSQLLLRVANAVSVKGIYKOMP 401
Db      342 FVSYSTFPFVSWRDPKSGSWYVETLDDIFEQWAGHSEDLSQLLLRVANAVSVKGIYKOMP 401

QY      402 GCENFLRKLLFFKTS 416
Db      402 GCENFLRKLLFFKTS 416

```

RESULT 10
 US-09-311-760-2
 ; Sequence 2, Application US/09311760
 ; Patent No. 6274318
 ; GENERAL INFORMATION:
 ; APPLICANT: Alnemri, Emad S.
 ; Fernandes-Alnemri, Teresa
 ; Litwack, Gerald
 ;
 ; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
 ; Encoding Same and Methods of Use
 ;
 ; NUMBER OF SEQUENCES: 87
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/311,760
 ; FILING DATE: 13-May-1999
 ; CLASSIFICATION: <Unknown>
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/665,579
 ; FILING DATE: <Unknown>
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-ID 2180
 ;
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-9849
 ;
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 416 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear

Db 222 QDHGALDCCVVILSHGQASHLQFPGAVYGTGDCPVSVEKIVNIFNGTSCPSLGGKPKL 281

QY 282 FFIQACGGEQKHGFVEASTSPEDSPGSGNPDPATPFQEGRLTFDQLDAISLPTPSDI 341

Db 282 FFIQACGGEQKHGFVEASTSPEDSPGSGNPDPATPFQEGRLTFDQLDAISLPTPSDI 341

QY 342 FVSYSTPFGFVSRDPSGWSYVETLDDIPEQWAHSEDLQSLLLRVANAVSVKGIYKOMP 401

Db 342 FVSYSTPFGFVSRDPSGWSYVETLDDIPEQWAHSEDLQSLLLRVANAVSVKGIYKOMP 401

QY 402 GCFNFKLKKLFFKTS 416

Db 402 GCFNFKLKKLFFKTS 416

RESULT 12

US-10-059-749-2

; Sequence 2, Application US/10059749

; Patent No. 6566505

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; Fernandes-Alnemri, Teresa

; Litwack, Gerald

; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids

; Encoding Same and Methods of Use

; NUMBER OF SEQUENCES: 87

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/059,749

; FILING DATE: 29-Jan-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/865,579

; FILING DATE: 29-MAY-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-ID 2180

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-9849

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 416 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-059-749-2

Query Match 46.9%; Score 195; DB 4; Length 416;

Best Local Similarity 100.0%; Pred. No. 1.1e-179; Indels 0; Gaps 0;

Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 QDHGALDCCVVILSHGQASHLQFPGAVYGTGDCPVSVEKIVNIFNGTSCPSLGGKPKL 281

Db 222 QDHGALDCCVVILSHGQASHLQFPGAVYGTGDCPVSVEKIVNIFNGTSCPSLGGKPKL 281

QY 282 FFIQACGGEQKHGFVEASTSPEDSPGSGNPDPATPFQEGRLTFDQLDAISLPTPSDI 341

Db 282 FFIQACGGEQKHGFVEASTSPEDSPGSGNPDPATPFQEGRLTFDQLDAISLPTPSDI 341

QY 222 QDHGALDCCVVILSHGQASHLQFPGAVYGTGDCPVSVEKIVNIFNGTSCPSLGGKPKL 281

Db 222 QDHGALDCCVVILSHGQASHLQFPGAVYGTGDCPVSVEKIVNIFNGTSCPSLGGKPKL 281

QY 282 FFIQACGGEQKHGFVEASTSPEDSPGSGNPDPATPFQEGRLTFDQLDAISLPTPSDI 341

Db 282 FFIQACGGEQKHGFVEASTSPEDSPGSGNPDPATPFQEGRLTFDQLDAISLPTPSDI 341

QY 342 FVSYSTPFGFVSRDPSGWSYVETLDDIPEQWAHSEDLQSLLLRVANAVSVKGIYKOMP 401

Db 342 FVSYSTPFGFVSRDPSGWSYVETLDDIPEQWAHSEDLQSLLLRVANAVSVKGIYKOMP 401

QY 402 GCFNFKLKKLFFKTS 416

Db 402 GCFNFKLKKLFFKTS 416

RESULT 11

US-08-865-579-2

; Sequence 2, Application US/08865579

; Patent No. 6455296

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; Fernandes-Alnemri, Teresa

; Litwack, Gerald

; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids

; Encoding Same and Methods of Use

; NUMBER OF SEQUENCES: 87

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/865,579

; FILING DATE: 29-MAY-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-ID 2180

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-9849

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 416 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-865-579-2

Query Match 46.9%; Score 195; DB 4; Length 416;

Best Local Similarity 100.0%; Pred. No. 1.1e-179; Indels 0; Gaps 0;

Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 QDHGALDCCVVILSHGQASHLQFPGAVYGTGDCPVSVEKIVNIFNGTSCPSLGGKPKL 281

QY 342 FVSYSTFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSKGIYKMP 401
 Db |||||
 QY 402 GCFNFKLFFKTS 416
 Db |||||

RESULT 13
 US-09-257-218-22
 ; Sequence 22, Application US/09257218
 ; Patent No. 6271361
 ; GENERAL INFORMATION:
 ; APPLICANT: Alnemri, Emad S.
 ; APPLICANT: Fernandes-Alnemri, Teresa
 ; APPLICANT: Litwack, Gerald
 ; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
 ; TITLE OF INVENTION: Encoding Same and Methods of Use
 ; NUMBER OF SEQUENCES: 87
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/257,218
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY INFORMATION:
 ; APPLICATION NUMBER: US/08/865,579
 ; FILING DATE: 29-MAY-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-ID 2180
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-9849
 ; INFORMATION FOR SEQ ID NO: 22:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE CHARACTERISTICS:
 ; INFORMATION FOR SEQ ID NO: 22:
 ; US-09-257-218-22

Query Match 3.6%; Score 15; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 350 GFVSWRDPKSGSWYV 364
 Db |||||
 1 GFVSWRDPKSGSWYV 15

RESULT 14
 US-09-311-760-22
 ; Sequence 22, Application US/09311760
 ; Patent No. 6274318
 ; GENERAL INFORMATION:
 ; APPLICANT: Alnemri, Emad S.
 ; APPLICANT: Fernandes-Alnemri, Teresa
 ; APPLICANT: Litwack, Gerald
 ; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
 ; TITLE OF INVENTION: Encoding Same and Methods of Use
 ; NUMBER OF SEQUENCES: 87
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/257,218
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY INFORMATION:
 ; APPLICATION NUMBER: US/08/865,579
 ; FILING DATE: 29-MAY-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-ID 2180
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-9849
 ; INFORMATION FOR SEQ ID NO: 22:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE CHARACTERISTICS:
 ; INFORMATION FOR SEQ ID NO: 22:
 ; US-09-257-218-22

Query Match 3.6%; Score 15; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 350 GFVSWRDPKSGSWYV 364
 Db |||||
 1 GFVSWRDPKSGSWYV 15

RESULT 15
 US-09-311-760-22
 ; Sequence 22, Application US/09311760
 ; Patent No. 6274318
 ; GENERAL INFORMATION:
 ; APPLICANT: Alnemri, Emad S.
 ; APPLICANT: Fernandes-Alnemri, Teresa
 ; APPLICANT: Litwack, Gerald
 ; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
 ; TITLE OF INVENTION: Encoding Same and Methods of Use
 ; NUMBER OF SEQUENCES: 87
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/311,760
 ; FILING DATE: 13-MAY-1999
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/865,579
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-ID 2180
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-9849
 ; INFORMATION FOR SEQ ID NO: 22:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE CHARACTERISTICS:
 ; INFORMATION FOR SEQ ID NO: 22:
 ; US-09-311-760-22

Query Match 3.6%; Score 15; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 350 GFVSWRDPKSGSWYV 364
 Db |||||
 1 GFVSWRDPKSGSWYV 15

RESULT 15
 US-09-561-756-59
 ; Sequence 59, Application US/09561756
 ; Patent No. 6376226
 ; GENERAL INFORMATION:
 ; APPLICANT: Alnemri, Emad S.
 ; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: 480140.431
 ; CURRENT APPLICATION NUMBER: US/09/561,756
 ; PRIOR FILING DATE: 2000-04-26
 ; PRIOR APPLICATION NUMBER: 09/227,721
 ; PRIOR FILING DATE: 1999-01-08
 ; NUMBER OF SEQ ID NOS: 116
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 59
 ; LENGTH: 15
 ; TYPE: PPT
 ; ORGANISM: Homo sapien
 ; US-09-561-756-59

Query Match 3.6%; Score 15; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 350 GFVSWRDPKSGSWYV 364
 Db |||||
 1 GFVSWRDPKSGSWYV 15

Best Local Similarity 100.0%; Pred. No. 2.1e-07; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 350 GFVSWRDPKSGSWYV 364
Db 1 GFVSWRDPKSGSWYV 15

RESULT 18
US-10-059-749-22
; Sequence 22, Application US/10059749
; Patent No. 6566505
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; Fernandes-Alnemri, Teresa
; Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESS: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/059,749
FILING DATE: 29-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-059-749-22

Query Match 3.6%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e-07; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 350 GFVSWRDPKSGSWYV 364
Db 1 GFVSWRDPKSGSWYV 15

RESULT 19
US-09-954-697-59
; Sequence 59, Application US/09954697
; Patent No. 6610541
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697

RESULT 16
US-09-227-721-59
; Sequence 59, Application US/09227721
; Patent No. 6379950
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/227,721
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-227-721-59

Query Match 3.6%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e-07; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 350 GFVSWRDPKSGSWYV 364
Db 1 GFVSWRDPKSGSWYV 15

RESULT 17
US-08-865-579-22
; Sequence 22, Application US/08865579
; Patent No. 6455296
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESS: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-865-579-22

Query Match 3.6%; Score 15; DB 4; Length 15;

; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-59

Query Match 3.6%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 GFVSWRDPKSGSWYV 364
Db 1 GFVSWRDPKSGSWYV 15

RESULT 20
US-09-257-218-6
; Sequence 6, Application US/09257218
; Patent No. 6271361
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,218
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997

; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-257-218-6

Query Match 3.6%; Score 15; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 GFVSWRDPKSGSWYV 364
Db 32 GFVSWRDPKSGSWYV 46

RESULT 21

US-09-311-760-6
; Sequence 6, Application US/09311760
; Patent No. 6274318
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/311,760
; FILING DATE: 13-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/865,579
; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-311-760-6
Query Match 3.6%; Score 15; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 GFVSWRDPKSGSWYV 364
Db 32 GFVSWRDPKSGSWYV 46

RESULT 22
US-08-865-579-6
; Sequence 6, Application US/08865579
; Patent No. 6455296
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:

TOPLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-059-749-6
Query Match 3.6%; Score 15; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 350 GFVSWRDPKSGSWYV 364
DB 32 GFVSWRDPKSGSWYV 46
RESULT 24
US-08-773-608A-2
; Sequence 2, Application US/08773608A
; Patent No. 5858778
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Sf Caspase-1, Compositions and Methods
; TITLE OF INVENTION: for Making and Methods of Using the Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5858778ris
; STREET: One Liberty Place 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: US
; ZIP: 19355
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/773.608A
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-2087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 299 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-773-608A-2
Query Match 2.6%; Score 11; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 277 GPKLFFFIQAC 287
DB 168 GPKLFFFIQAC 178
RESULT 25
US-09-187-789-38
; Sequence 38, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
MOLECULE TYPE: peptide
US-08-865-579-6
Query Match 3.6%; Score 15; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 350 GFVSWRDPKSGSWYV 364
DB 32 GFVSWRDPKSGSWYV 46
RESULT 23
US-10-059-749-6
; Sequence 6, Application US/10059749
; Patent No. 6566505
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid

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/ TITLE OF INVENTION: AND METHODS OF USE
/ FILE REFERENCE: 480140.434C1
/ CURRENT APPLICATION NUMBER: US/09/187,789
/ CURRENT FILING DATE: 1998-11-06
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 38
/ LENGTH: 39
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-187-789-38

Query Match          2.4%; Score 10; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPXLFFFIQAC 287
Db 21 KPXLFFFIQAC 30

RESULT 26
US-09-139-600-33
/ Sequence 33, Application US/09139600
/ Patent No. 6432628
/ GENERAL INFORMATION:
/ APPLICANT: Alnemri, Emad S.
/ APPLICANT: Fernandez-Alnemri, Teresa
/ TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
/ FILE REFERENCE: 480140.434
/ CURRENT APPLICATION NUMBER: US/09/139,600
/ CURRENT FILING DATE: 1998-08-25
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 33
/ LENGTH: 39
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-139-600-33

Query Match          2.4%; Score 10; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPXLFFFIQAC 287
Db 21 KPXLFFFIQAC 30

RESULT 27
US-08-462-969B-2
/ Sequence 2, Application US/08462969B
/ Patent No. 6087150
/ GENERAL INFORMATION:
/ APPLICANT: He, Wei-Wu et al.
/ TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
/ TITLE OF INVENTION: Like Apoptosis Protease 3 and 4
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Human Genome Sciences, Inc.
/ STREET: 9410 Key West Ave.
/ CITY: Rockville
/ STATE: MD
/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/462,969B
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/ FILING DATE: 05-JUN-1995
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/334,251
/ FILING DATE: 11-NOV-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Brookes, A. Anders
/ REGISTRATION NUMBER: 36,373
/ REFERENCE/DOCKET NUMBER: PF140P1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 301-309-8504
/ TELEFAX: 301-309-8439
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 303 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-462-969B-2

Query Match          2.4%; Score 10; DB 3; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPXLFFFIQAC 287
Db 177 KPXLFFFIQAC 186

RESULT 28
US-09-561-756-24
/ Sequence 24, Application US/09561756
/ Patent No. 6376226
/ GENERAL INFORMATION:
/ APPLICANT: Alnemri, Emad S.
/ TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: 480140.431
/ CURRENT APPLICATION NUMBER: US/09/561,756
/ CURRENT FILING DATE: 2000-04-26
/ PRIOR APPLICATION NUMBER: 09/227,721
/ PRIOR FILING DATE: 1999-01-08
/ NUMBER OF SEQ ID NOS: 116
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 24
/ LENGTH: 303
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-09-561-756-24

Query Match          2.4%; Score 10; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPXLFFFIQAC 287
Db 177 KPXLFFFIQAC 186

RESULT 29
US-09-227-721-24
/ Sequence 24, Application US/09227721
/ Patent No. 6379950
/ GENERAL INFORMATION:
/ APPLICANT: Alnemri, Emad S.
/ TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: 480140.431
/ CURRENT APPLICATION NUMBER: US/09/227,721
/ CURRENT FILING DATE: 1999-01-08
/ NUMBER OF SEQ ID NOS: 116
/ SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 24
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-227-721-24

Query Match          2.4%; Score 10; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      278 KPCLFFFIQAC 287
Db      177 KPCLFFFIQAC 186
|||||

RESULT 30
US-09-556-627A-2
; Sequence 2, Application US/08556627A
; Patent No. 6462175
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch3, A No. 6462175el Apoptotic Protease,
; TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,627A
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1813
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-556-627A-2

Query Match          2.4%; Score 10; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      278 KPCLFFFIQAC 287
Db      177 KPCLFFFIQAC 186
|||||

RESULT 31
US-09-124-934A-2
; Sequence 2, Application US/09124934A
; Patent No. 6495519
; GENERAL INFORMATION:
```

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; APPLICANT: He, Wei-Wu et al.,
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme Like Apoptosis Protease 3 a
; FILE REFERENCE: PF140C1
; CURRENT APPLICATION NUMBER: US/09/124,934A
; CURRENT FILING DATE: 1994-11-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 303
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-124-934A-2

Query Match          2.4%; Score 10; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      278 KPCLFFFIQAC 287
Db      177 KPCLFFFIQAC 186
|||||

RESULT 32
US-08-724-378D-4
; Sequence 4, Application US/08724378D
; Patent No. 6512104
; GENERAL INFORMATION:
; APPLICANT: JUAN, SHAO-CHIEH
; APPLICANT: FLETCHER, FREDERICK A.
; APPLICANT: PATTERSON, SCOTT D.
; TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE
; FILE REFERENCE: 06843-0019-00000
; CURRENT APPLICATION NUMBER: US/08/724,378D
; CURRENT FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-724-378D-4

Query Match          2.4%; Score 10; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      278 KPCLFFFIQAC 287
Db      177 KPCLFFFIQAC 186
|||||

RESULT 33
US-08-334-251D-2
; Sequence 2, Application US/08334251D
; Patent No. 6538121
; GENERAL INFORMATION:
; APPLICANT: He et al.,
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme Like Apoptosis Protease 3 a
; FILE REFERENCE: PF140
; CURRENT APPLICATION NUMBER: US/08/334,251D
; CURRENT FILING DATE: 1994-11-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-334-251D-2

Query Match          2.4%; Score 10; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 278 KPKLFFFIQAC 287
    |||||
Db 177 KPKLFFFIQAC 186

RESULT 34
US-09-954-697-24
; Sequence 24, Application US/09954697
; Patent No. 6610541
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-24

Query Match 2.4%; Score 10; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFFIQAC 287
    |||||
Db 177 KPKLFFFIQAC 186

RESULT 35
US-09-163-099-2
; Sequence 2, Application US/09163099
; Patent No. 6686459
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch3, A No. 6686459el Apoptotic Protease,
; TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/163,099
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/556,627
; FILING DATE: 13-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1813
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-8941
; TELEFAX: (619) 535-8949

QY 278 KPKLFFFIQAC 287
    |||||
Db 177 KPKLFFFIQAC 186

RESULT 36
US-08-618-408B-2
; Sequence 2, Application US/08618408B
; Patent No. 5851815
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch4 and Mch5, No. 5851815el Apoptotic
; TITLE OF INVENTION: Proteases, Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,408B
; FILING DATE: 19-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1957
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-618-408B-2

Query Match 2.4%; Score 10; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFFIQAC 287
    |||||
Db 216 KPKLFFFIQAC 225

RESULT 37
US-08-724-378D-2
; Sequence 2, Application US/08724378D
```

```
; Patent No. 6512104
; GENERAL INFORMATION:
; APPLICANT: JUAN, SHAO-CHIEH
; APPLICANT: FLETCHER, FREDERICK A.
; APPLICANT: PATTERSON, SCOTT D.
; TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE
; TITLE OF INVENTION: PROTEASE
; FILE REFERENCE: 06843-0019-00000
; CURRENT APPLICATION NUMBER: US/08/724,378D
; CURRENT FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-724-378D-2

Query Match 2.4%; Score 10; DB 4; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.25; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 278 KPCLFFFIQAC 287
| | | | | | | |
DB 259 KPCLFFFIQAC 268

RESULT 38
US-08-724-378D-3
; Sequence 3, Application US/08724378D
; Patent No. 6512104
; GENERAL INFORMATION:
; APPLICANT: JUAN, SHAO-CHIEH
; APPLICANT: FLETCHER, FREDERICK A.
; APPLICANT: PATTERSON, SCOTT D.
; TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE
; TITLE OF INVENTION: PROTEASE
; FILE REFERENCE: 06843-0019-00000
; CURRENT APPLICATION NUMBER: US/08/724,378D
; CURRENT FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-724-378D-3

Query Match 2.4%; Score 10; DB 4; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.25; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 278 KPCLFFFIQAC 287
| | | | | | | |
DB 259 KPCLFFFIQAC 268

RESULT 39
US-08-665-220-2
; Sequence 2, Application US/08665220
; Patent No. 5786173
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,
; TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
```

```
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,220
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/618,408
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 479 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-665-220-2

Query Match 2.4%; Score 10; DB 1; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.3; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 278 KPCLFFFIQAC 287
| | | | | | | |
DB 349 KPCLFFFIQAC 358

RESULT 40
US-09-291-692-2
; Sequence 2, Application US/09291692
; Patent No. 6287795
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING AND METHODS OF USE
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: Use
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/291,692
; FILING DATE: 04-13-1999
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 480140.424C3
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-291-692-2

Query Match 2.4%; Score 10; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
|||||
Db 349 KPCLFFFIQAC 358

RESULT 41
US-09-561-756-33
Sequence 33, Application US/09561756
Patent No. 6376226
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/561.756
CURRENT FILING DATE: 2000-04-26
PRIOR FILING DATE: 09/227,721
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapien
US-09-561-756-33

Query Match 2.4%; Score 10; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
|||||
Db 349 KPCLFFFIQAC 358

RESULT 42
US-09-227-721-33
Sequence 33, Application US/09227721
Patent No. 6379950
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/227,721
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapien
US-09-227-721-33

Query Match 2.4%; Score 10; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
|||||
Db 349 KPCLFFFIQAC 358

RESULT 43
US-09-954-697-33
Sequence 33, Application US/09954697
Patent No. 6610541
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
FILE REFERENCE: 480140.431D2
CURRENT APPLICATION NUMBER: US/09/954.697
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapien
US-09-954-697-33

Query Match 2.4%; Score 10; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
|||||
Db 349 KPCLFFFIQAC 358

RESULT 44
US-09-009-893A-4
Sequence 4, Application US/09009893A
Patent No. 6623938
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Dixit, Vishva M.
APPLICANT: Gentz, Reiner L.
APPLICANT: Kenny, Joseph J.
TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Rec
FILE REFERENCE: 1488.0970002
CURRENT APPLICATION NUMBER: US/09/009,893A
CURRENT FILING DATE: 1998-02-21
PRIOR APPLICATION NUMBER: US 60/054,800
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/034,205
PRIOR FILING DATE: 1997-01-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapiens
US-09-009-893A-4

Query Match 2.4%; Score 10; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
|||||
Db 349 KPCLFFFIQAC 358

RESULT 45
US-09-489-155-4
Sequence 4, Application US/09489155
Patent No. 6680171

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-962-834A-2

Query Match 2.4%; Score 10; DB 4; Length 521;
Best Local Similarity 100.0%; Pred. No. 0.32; Indels 0;
Matches 10; Conservative 0; Mismatches 0; Gaps 0;

QY 278 KPKLFFFIQAC 287
Db 392 KPKLFFFIQAC 401

RESULT 47
US-09-257-218-19
; Sequence 19, Application US/09257218
; Patent No. 6271361
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/257,218
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-257-218-19

Query Match 2.2%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 FTQACGGEQ 291
Db 1 FTQACGGEQ 9

RESULT 48
US-09-311-760-19
; Sequence 19, Application US/09311760
; Patent No. 6274318
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa

GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: 1-FLICE, A No. 6680171el Inhibitor of Tumor Necrosis Factor Recep
; TITLE OF INVENTION: CD-95 Induced Apoptosis
; FILE REFERENCE: 1488.0970002
; CURRENT APPLICATION NUMBER: US/09/489,155
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/009,893
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-155-4

Query Match 2.4%; Score 10; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.3; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFFIQAC 287
Db 349 KPKLFFFIQAC 358

RESULT 46
US-09-962-834A-2
; Sequence 2, Application US/09962834A
; Patent No. 6586225
; GENERAL INFORMATION:
; APPLICANT: Bowman, Michael
; TITLE OF INVENTION: NOVEL PROTEASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/962,834A
; FILING DATE: 25-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,123
; FILING DATE: 1996-07-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: C15276
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 521 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein

;; Litwack, Gerald
;; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
;; NUMBER OF SEQUENCES: 87
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Campbell & Flores LLP
;; STREET: 4370 La Jolla Village Drive, Suite 700
;; CITY: San Diego
;; STATE: California
;; COUNTRY: United States
;; ZIP: 92122
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/311,760
;; FILING DATE: 13-May-1999
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/865,579
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-ID 2180
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-9849
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-311-760-19

Query Match 2.2%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 FIQACGGEQ 291
Db 1 FIQACGGEQ 9

RESULT 49
US-09-561-756-56
; Sequence 56, Application US/09561756
; Patent No. 6376226
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/561,756
; CURRENT FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 09/227,721
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-561-756-56

Query Match 2.2%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 FIQACGGEQ 291
Db 1 FIQACGGEQ 9
RESULT 50
US-09-227-721-56
; Sequence 56, Application US/09227721
; Patent No. 6379950
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/227,721
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-227-721-56

Query Match 2.2%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 FIQACGGEQ 291
Db 1 FIQACGGEQ 9

Search completed: August 3, 2004, 09:11:41
Job time : 20 secs

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; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954.697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-30

Query Match      52.6%; Score 219; DB 9; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.7e-199;
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 HFMEVVKGDLTAKKMWLALALALARQDHGALDCCVVVILSHGCGQASHLQFPGAVYGTGDCP 257
DB 198 HFMEVVKGDLTAKKMWLALALALARQDHGALDCCVVVILSHGCGQASHLQFPGAVYGTGDCP 257
QY 258 VSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKHGFVASTSPDESFGSNPEPDAT 317
DB 258 VSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKHGFVASTSPDESFGSNPEPDAT 317
QY 318 PFQGLRTFDQDLSSTLPTSDIFVSYSTPPGFVSWRDPKSGSWYVETLDDIFEQWAHS 377
DB 318 PFQGLRTFDQDLSSTLPTSDIFVSYSTPPGFVSWRDPKSGSWYVETLDDIFEQWAHS 377
QY 378 EDLQSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
DB 378 EDLQSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 2
US-10-068-569-1
; Sequence 1, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-1

Query Match      52.6%; Score 219; DB 13; Length 416;
Best Local Similarity 99.7%; Pred. No. 1.7e-199;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 97 KLSKPTLENLTPVLRPEIRKPEVLRPETPRPVDIGSGGFDVGALSLRGNADLAYILS 156
DB 97 KLSKPTLENLTPVLRPEIRKPEVLRPETPRPVDIGSGGFDVGALSLRGNADLAYILS 156
QY 157 MEPCGHCLINNVNFCRESGLRTRTGSNDCEKLRFRFSLHFMVVKGLDTAKKMWLAL 216
DB 157 MEPCGHCLINNVNFCRESGLRTRTGSNDCEKLRFRFSLHFMVVKGLDTAKKMWLAL 216
QY 217 LELARQDHGALDCCVVVILSHGCGQASHLQFPGAVYGTGDCPVSVKIVNIFNGTSCPSLG 276
DB 217 LELAQDHGALDCCVVVILSHGCGQASHLQFPGAVYGTGDCPVSVKIVNIFNGTSCPSLG 276
QY 277 GKPKLFFIQACGGEQKHGFVASTSPDESFGSNPEPDATPQEGRLTFDQDLSLSP 336
DB 277 GKPKLFFIQACGGEQKHGFVASTSPDESFGSNPEPDATPQEGRLTFDQDLSLSP 336
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QY 337 TPSDIFVSYSTFPFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGI 396
DB 337 TPSDIFVSYSTFPFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGI 396
QY 397 YKQMPGCFNLRKKLFFKTS 416
DB 397 YKQMPGCFNLRKKLFFKTS 416

RESULT 3
US-09-851-873-102
; Sequence 102, Application US/09851873
; Publication No. US20030165488A1
; GENERAL INFORMATION:
; APPLICANT: Kletzien, Rolf F
; APPLICANT: Reardon, Ilene M
; APPLICANT: Welland, Katherine L
; TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
; FILE REFERENCE: 28341/00233
; CURRENT APPLICATION NUMBER: US/09/851,873
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 102
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-873-102

Query Match      46.9%; Score 195; DB 10; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.2e-176;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 QDHGALDCCVVVILSHGCGQASHLQFPGAVYGTGDCPVSVKIVNIFNGTSCPSLGGKPKL 281
DB 222 QDHGALDCCVVVILSHGCGQASHLQFPGAVYGTGDCPVSVKIVNIFNGTSCPSLGGKPKL 281
QY 282 FFIQACGGEQKHGFVASTSPDESFGSNPEPDATPQEGRLTFDQDLSLTPSDI 341
DB 282 FFIQACGGEQKHGFVASTSPDESFGSNPEPDATPQEGRLTFDQDLSLTPSDI 341
QY 342 FVSYSTFPFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKOMP 401
DB 342 FVSYSTFPFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKOMP 401
QY 402 GCFNLRKKLFFKTS 416
DB 402 GCFNLRKKLFFKTS 416

RESULT 4
US-09-746-731-2
; Sequence 2, Application US/09746731
; Publication No. US20010016345A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/746,731
/ FILING DATE: 22-Dec-2000
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/865,579
/ FILING DATE: 29-MAY-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-ID 2180
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-9849
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 416 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-746-731-2

Query Match          46.9%; Score 195; DB 12; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.2e-176;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 QDHGALDCCVVILSHGCOASHLQPPGAVYGTDCGPVSVKEIVNIFNGTSCPSLGGKPKL 281
Db 222 QDHGALDCCVVILSHGCOASHLQPPGAVYGTDCGPVSVKEIVNIFNGTSCPSLGGKPKL 281
QY 282 FFIQACGGEQKDHGFVASTSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTPSDI 341
Db 282 FFIQACGGEQKDHGFVASTSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTPSDI 341
QY 342 FVSYSTPFGFVSRDPRKSGWYVETLDDIPEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
Db 342 FVSYSTPFGFVSRDPRKSGWYVETLDDIPEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
QY 402 GCFNFKLKKLFKTS 416
Db 402 GCFNFKLKKLFKTS 416
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```
RESULT 5
US-10-059-749-2
/ Sequence 2, Application US/10059749
/ Publication No. US20020183504A1
/ GENERAL INFORMATION:
/ APPLICANT: Alnemri, Emad S.
/               Fernandes-Alnemri, Teresa
/               Litwack, Gerald
/ TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
/               Encoding Same and Methods of Use
/ NUMBER OF SEQUENCES: 87
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Campbell & Flores LLP
/ STREET: 4370 La Jolla Village Drive, Suite 700
/ CITY: San Diego
/ STATE: California
/ COUNTRY: United States
/ ZIP: 92122
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/059,749
/ FILING DATE: 29-Jan-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/865,579
```

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/
/ FILING DATE: 29-MAY-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-ID 2180
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-9849
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 416 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-059-749-2

Query Match          46.9%; Score 195; DB 13; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.2e-176;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 QDHGALDCCVVILSHGCOASHLQPPGAVYGTDCGPVSVKEIVNIFNGTSCPSLGGKPKL 281
Db 222 QDHGALDCCVVILSHGCOASHLQPPGAVYGTDCGPVSVKEIVNIFNGTSCPSLGGKPKL 281
QY 282 FFIQACGGEQKDHGFVASTSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTPSDI 341
Db 282 FFIQACGGEQKDHGFVASTSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTPSDI 341
QY 342 FVSYSTPFGFVSRDPRKSGWYVETLDDIPEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
Db 342 FVSYSTPFGFVSRDPRKSGWYVETLDDIPEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
QY 402 GCFNFKLKKLFKTS 416
Db 402 GCFNFKLKKLFKTS 416
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RESULT 6
US-10-141-618-4
/ Sequence 4, Application US/10141618
/ Publication No. US20030165887A1
/ GENERAL INFORMATION:
/ APPLICANT: Reed, John C.
/ TITLE OF INVENTION: Methods For Determining the Prognosis
/ FILE OF INVENTION: For Cancer Patients Using Tucan
/ FILE REFERENCE: P-LJ 5254
/ CURRENT APPLICATION NUMBER: US/10/141,618
/ CURRENT FILING DATE: 2002-05-07
/ PRIOR APPLICATION NUMBER: US 60/289,233
/ PRIOR FILING DATE: 2001-05-07
/ PRIOR APPLICATION NUMBER: US 60/356,934
/ PRIOR FILING DATE: 2002-02-12
/ PRIOR APPLICATION NUMBER: US 09/388,221
/ PRIOR FILING DATE: 1999-09-01
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 416
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-141-618-4

Query Match          46.9%; Score 195; DB 14; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.2e-176;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 QDHGALDCCVVILSHGCOASHLQPPGAVYGTDCGPVSVKEIVNIFNGTSCPSLGGKPKL 281
Db 222 QDHGALDCCVVILSHGCOASHLQPPGAVYGTDCGPVSVKEIVNIFNGTSCPSLGGKPKL 281
QY 282 FFIQACGGEQKDHGFVASTSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTPSDI 341
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Db 282 FFIAQCGEKDGHGFEVASTSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTSDI 341
Qy 342 FVSYSTPPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKMP 401
Db 342 FVSYSTPPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKMP 401
Qy 402 GCFNFKLKKLFFKTS 416
Db 402 GCFNFKLKKLFFKTS 416

RESULT 7
US-10-116-275-172
; Sequence 172, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'hahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrnie, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-172

Query Match 30.5%; Score 127; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 4e-112;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 290 EQKDHGFEVASTSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTFP 349
Db 140 EQKDHGFEVASTSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTFP 199
Qy 350 GFVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKMPGCCFNFLK 409
Db 200 GFVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKMPGCCFNFLK 259
Qy 410 KLFKTS 416
Db 260 KLFKTS 266

RESULT 8
US-10-014-269-27
; Sequence 27, Application US/10014269
; Publication No. US2002012673A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogura, Yasunori
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06645
; CURRENT APPLICATION NUMBER: US/10/014,269
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-269-27

Query Match 22.4%; Score 93; DB 13; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.5e-80;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 3.5e-80;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLVBEQLQVDLWDVLLSRELFRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRLRCRLVBEQLQVDLWDVLLSRELFRPHMIEDIQAGSGSRDQARQLII 60
Qy 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNR 93
Db 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNR 93

RESULT 9
US-10-002-974-27
; Sequence 27, Application US/10002974
; Publication No. US20020197616A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogura, Yasunori
; APPLICANT: Cho, Judy
; APPLICANT: Nicolae, Dan L
; APPLICANT: Bonen, Denise
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06646
; CURRENT APPLICATION NUMBER: US/10/002,974
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-974-27

Query Match 22.4%; Score 93; DB 13; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.5e-80;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLVBEQLQVDLWDVLLSRELFRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRLRCRLVBEQLQVDLWDVLLSRELFRPHMIEDIQAGSGSRDQARQLII 60
Qy 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNR 93
Db 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNR 93

RESULT 10
US-10-314-506-27
; Sequence 27, Application US/10314506
; Publication No. US20030175762A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogura, Yasunori
; TITLE OF INVENTION: Modulators of NOD2 Signaling
; FILE REFERENCE: UM-06984
; CURRENT APPLICATION NUMBER: US/10/314,506
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 10,014,269
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/244,289
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-314-506-27

Query Match 22.4%; Score 93; DB 14; Length 93;

Best Local Similarity	100.0%;	Pred. No. 3.5e-80;
Matches	93; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MDEADRLRRCRLVEELVEEQDQLWDVLLSRELFRPHMIEDIQAGSGSRDDAQLII 60
Db	1 MDEADRLRRCRLVEELVEEQDQLWDVLLSRELFRPHMIEDIQAGSGSRDDAQLII 60

Qy 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNR 93
|||
Db 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNR 93

```

RESULT 11
US-10-424-599-174531
; Sequence 174531, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovacic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 174531
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_12861C.1.pep
US-10-424-599-174531

```

Query Match 16.6%; Score 69; DB 12; Length 159;
Best Local Similarity 100.0%; Pred. No. 3.9e-57;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	12	CRRLRV	VEELQV	QDQLWD	VLLSREL	FRPHMIEDI	QRAGSGRR	DDQARQLIID	LETFGSQALP	71
Db	12	CRRLRV	VEELQV	QDQLWD	VLLSREL	FRPHMIEDI	QRAGSGRR	DDQARQLIID	LETFGSQALP	71

Qy 72 LFISCLDT 80
Db 72 LFISCLDT 80

```

RESULT 12
US-10-153-344-26
; Sequence 26, Application US/10153344
; Publication No. US2003000412A1
; GENERAL INFORMATION:
; APPLICANT: ROTHMAN, JOEL
; APPLICANT: BLOSS, TIM
; APPLICANT: WITZE, ERIC
; TITLE OF INVENTION: BTF3: AN INHIBITOR OF APOPTOSIS
; FILE REFERENCE: 407T-300410US
; CURRENT APPLICATION NUMBER: US/10/153,344
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/292,559
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-153-344-26

```

```
Query Match      10.1%; Score 42; DB 14; Length 42;
Best Local Similarity 100.0%; Pred. No. 5.8e-32;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 47 GSGRRDQARQLIIDLETRGSQALPLFISCLEDTGQDMLASF 88
Db 1 GSGRRDQARQLIIDLETRGSQALPLFISCLEDTGQDMLASF 42

```

RESULT 13
US-10-068-569-18
; Sequence 18, Application US/10068569
; Publication NO. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-18

```

```
Query Match          7.7%; Score 32; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	303	PEDESPGNPEPDATPFQEGRLTFDQLDAISS	334
Db	1	PEDESPGNPEPDATPFQEGRLTFDQLDAISS	32

```

RESULT 14
US-10-068-569-22
; Sequence 22, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-22

```

```

Query Match      7.7%; Score 32; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 PEDESGNSPEPDATPFQEGRLTFDQDAISS 334
DB 1 PEDESGNSPEPDATPFQEGRLTFDQDAISS 32

```

RESULT 15
US-10-153-344-16
; Sequence 16, Application US/10153344
; Publication No. US20030004124A1
; GENERAL INFORMATION:
; APPLICANT: ROTHMAN, JOEL
; APPLICANT: BLOSS, TIM

```
; APPLICANT: WITZE, ERIC
; TITLE OF INVENTION: BTF3: AN INHIBITOR OF APOPTOSIS
; FILE REFERENCE: 407T-300410US
; CURRENT APPLICATION NUMBER: US/10/153,344
; PRIOR FILING DATE: 2002-08-27
; CURRENT APPLICATION NUMBER: US 60/292,559
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 16
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-10-153-344-16

Query Match          4.6%; Score 19; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 WDVLLSRELPRPHMIEDIQ 44
Db 1 WDVLLSRELPRPHMIEDIQ 19

RESULT 16
US-09-954-697-59
; Sequence 59, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-954-697-59

Query Match          3.6%; Score 15; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 350 GFVSWRDPKSGSWYV 364
Db 1 GFVSWRDPKSGSWYV 15

RESULT 17
US-09-746-731-22
; Sequence 22, Application US/09746731
; Publication No. US20010016345A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
;               Fernandes-Alnemri, Teresa
;               Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
;               Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; APPLICANT: WITZE, ERIC
; TITLE OF INVENTION: BTF3: AN INHIBITOR OF APOPTOSIS
; FILE REFERENCE: 407T-300410US
; CURRENT APPLICATION NUMBER: US/10/153,344
; PRIOR FILING DATE: 2002-08-27
; CURRENT APPLICATION NUMBER: US 60/292,559
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 16
; LENGTH: 19
; TYPE: PRT
; ORGANISM: PC-DOS/MS-DOS
; US-09-746-731-22

Query Match          3.6%; Score 15; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 350 GFVSWRDPKSGSWYV 364
Db 1 GFVSWRDPKSGSWYV 15

RESULT 18
US-10-068-569-6
; Sequence 6, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-068-569-6

Query Match          3.6%; Score 15; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 316 ATPFOEGLRTFDQLD 330
Db 1 ATPFOEGLRTFDQLD 15

RESULT 19
US-10-068-569-11
; Sequence 11, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
```

```
; TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-11

Query Match          3.6%; Score 15; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 ATPFQEGRLTFDQLD 330
Db 1 ATPFQEGRLTFDQLD 15

RESULT 20
US-10-059-749-22
; Sequence 22, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-059-749-22

Query Match          3.6%; Score 15; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 GFVSWRDPKSGSWYV 364
Db 1 GFVSWRDPKSGSWYV 15

RESULT 21
US-10-174-105A-131
; Sequence 131, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 131
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: MOD RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 10 is phosphorylated
US-10-174-105A-131

Query Match          3.6%; Score 15; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 CEKLRRRFSSSLHFMV 201
Db 1 CEKLRRRFSSSLHFMV 15

RESULT 22
US-10-174-105A-132
; Sequence 132, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 132
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-174-105A-132

Query Match          3.6%; Score 15; DB 14; Length 15;
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Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 CEKLRFRFSSLHFVW 201
Db 1 CEKLRFRFSSLHFVW 15

RESULT 23
US-10-174-105A-176
; Sequence 176, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 176
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetic Peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 10 is phosphorylated
US-10-174-105A-176

Query Match 3.6%; Score 15; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 CEKLRFRFSSLHFVW 201
Db 1 CEKLRFRFSSLHFVW 15

RESULT 24
US-10-197-634-7
; Sequence 7, Application US/10197634
; Publication No. US20030073629A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: OMI AND DOMAINS THEREOF THAT DISRUPT
; FILE REFERENCE: 480140.479
; CURRENT APPLICATION NUMBER: US/10/197,634
; CURRENT FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-197-634-7

Query Match 3.6%; Score 15; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 ATPFQGLRTFDQLD 330

Db 1 ATPFQGLRTFDQLD 15

RESULT 25
US-09-746-731-6
; Sequence 6, Application US/09746731
; Publication No. US20010016345A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/746,731
; FILING DATE: 22-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-3849
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-746-731-6

Query Match 3.6%; Score 15; DB 12; Length 46;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 GFVSWRDPKSGSWYV 364
Db 32 GFVSWRDPKSGSWYV 46

RESULT 26
US-10-059-749-6
; Sequence 6, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/059,749
FILING DATE: 29-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/865,579
FILING DATE: 29-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 2180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9849
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-059-749-6

Query Match 3.8%; Score 15; DB 13; Length 46;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 GFVSWRDPKSGSWYV 364
DB 32 GFVSWRDPKSGSWYV 46

RESULT 27
US-10-174-105A-133
; Sequence 133, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 133
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: MOD RES
; LOCATION: (10)..(10)
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 10 is phosphorylated
US-10-174-105A-133

Query Match 2.9%; Score 12; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 SGLRTRTGSNID 186
DB 2 SGLRTRTGSNID 13

RESULT 28
US-10-174-105A-134
; Sequence 134, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-174-105A-134

Query Match 2.9%; Score 12; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 SGLRTRTGSNID 186
DB 2 SGLRTRTGSNID 13

RESULT 29
US-10-153-344-17
; Sequence 17, Application US/10153344
; Publication No. US20030004124A1
; GENERAL INFORMATION:
; APPLICANT: ROTHMAN, JOEL
; APPLICANT: BLOSS, TIM
; APPLICANT: WITZE, ERIC
; TITLE OF INVENTION: BTF3: AN INHIBITOR OF APOPTOSIS
; FILE REFERENCE: 407T-300410US
; CURRENT APPLICATION NUMBER: US/10/153,344
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/292,559
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-153-344-17

Query Match 2.4%; Score 10; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 RDQARQLIID 61


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/ STREET: 9410 Key West Ave.
/ CITY: Rockville
/ STATE: MD
/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/895,263
/ FILING DATE: 02-Jul-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: <Unknown>
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jonathan L. Klein
/ REGISTRATION NUMBER: 41,119
/ REFERENCE/DOCKET NUMBER: PF140
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 301-251-6015
/ TELEFAX: 301-309-8439
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 303 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-895-263-2

Query Match 2.4%; Score 10; DB 9; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFIQAC 287
Db 177 KPKLFFIQAC 186

RESULT 34
US-09-944-851-2
/ Sequence 2, Application US/09944851
/ Patent No. US20020102648A1
/ GENERAL INFORMATION:
/ APPLICANT: Alnemri, Emad S.
/ FERNANDES-ALNEMRI, TERESA
/ Litwack, Gerald
/ Armstrong, Robert
/ Tomaselli, Kevin
/ TITLE OF INVENTION: Mch3, A No. US20020102648A1el Apoptotic Protease,
/ Nucleic Acids Encoding and Methods of Use
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Campbell and Flores
/ STREET: 4370 La Jolla Village Drive, Suite 700
/ CITY: San Diego
/ STATE: California
/ COUNTRY: USA
/ ZIP: 92122
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/944,851
/ FILING DATE: 31-Aug-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
```

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/ APPLICATION NUMBER: 09/556,627
/ FILING DATE: 13-NOV-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-ID 1813
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 303 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-944-851-2

Query Match 2.4%; Score 10; DB 9; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFIQAC 287
Db 177 KPKLFFIQAC 186

RESULT 35
US-09-954-697-24
/ Sequence 24, Application US/09954697
/ Patent No. US20020106631A1
/ GENERAL INFORMATION:
/ APPLICANT: Alnemri, Emad S.
/ TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
/ FILE REFERENCE: 480140.431D2
/ CURRENT APPLICATION NUMBER: US/09/954,697
/ CURRENT FILING DATE: 2001-09-14
/ NUMBER OF SEQ ID NOS: 116
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 24
/ LENGTH: 303
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-09-954-697-24

Query Match 2.4%; Score 10; DB 9; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFIQAC 287
Db 177 KPKLFFIQAC 186

RESULT 36
US-09-851-873-100
/ Sequence 100, Application US/09851873
/ Publication No. US20030165488A1
/ GENERAL INFORMATION:
/ APPLICANT: Kietzien, Rolf F
/ APPLICANT: Reardon, Ilene M
/ APPLICANT: Weiland, Katherine L
/ TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
/ FILE REFERENCE: 28341/00233
/ CURRENT APPLICATION NUMBER: US/09/851,873
/ CURRENT FILING DATE: 2001-05-08
/ NUMBER OF SEQ ID NOS: 105
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 100
/ LENGTH: 303
/ TYPE: PRT
/ ORGANISM: Homo sapiens
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US-09-851-873-100

Query Match 2.4%; Score 10; DB 10; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
|||||
Db 177 KPCLFFFIQAC 186

RESULT 37

US-10-337-060-2
; Sequence 2, Application US/10337060
; Publication No. US20030119169A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: MCH3, A NOVEL APOPTOTIC PROTEASE,
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING AND METHODS OF USE
; FILE REFERENCE: 480140.423D2
; CURRENT APPLICATION NUMBER: US/10/337,060
; CURRENT FILING DATE: 2003-01-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-337-060-2

Query Match 2.4%; Score 10; DB 14; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
|||||
Db 177 KPCLFFFIQAC 186

RESULT 38

US-10-280-670-4
; Sequence 4, Application US/10280670
; Publication No. US20030170812A1
; GENERAL INFORMATION:
; APPLICANT: JUAN, SHAO-CHIEH
; APPLICANT: FLETCHER, FREDERICK A.
; APPLICANT: PATTERSON, SCOTT D.
; TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE
; TITLE OF INVENTION: PROTEASE
; FILE REFERENCE: 06843-0019-01000
; CURRENT APPLICATION NUMBER: US/10/280,670
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 08/724,378
; PRIOR FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-280-670-4

Query Match 2.4%; Score 10; DB 14; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
|||||
Db 177 KPCLFFFIQAC 186

RESULT 39

US-10-280-670-2
; Sequence 2, Application US/10280670
; Publication No. US20030170812A1
; GENERAL INFORMATION:
; APPLICANT: JUAN, SHAO-CHIEH
; APPLICANT: FLETCHER, FREDERICK A.
; APPLICANT: PATTERSON, SCOTT D.
; TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE
; TITLE OF INVENTION: PROTEASE
; FILE REFERENCE: 06843-0019-01000
; CURRENT APPLICATION NUMBER: US/10/280,670
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 08/724,378
; PRIOR FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-280-670-2

Query Match 2.4%; Score 10; DB 14; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
|||||
Db 259 KPCLFFFIQAC 268

RESULT 40

US-10-280-670-3
; Sequence 3, Application US/10280670
; Publication No. US20030170812A1
; GENERAL INFORMATION:
; APPLICANT: JUAN, SHAO-CHIEH
; APPLICANT: FLETCHER, FREDERICK A.
; APPLICANT: PATTERSON, SCOTT D.
; TITLE OF INVENTION: INTERLEUKIN 1-BETA CONVERTING ENZYME LIKE CYSTEINE
; TITLE OF INVENTION: PROTEASE
; FILE REFERENCE: 06843-0019-01000
; CURRENT APPLICATION NUMBER: US/10/280,670
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 08/724,378
; PRIOR FILING DATE: 1996-10-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-280-670-3

Query Match 2.4%; Score 10; DB 14; Length 389;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
|||||
Db 259 KPCLFFFIQAC 268

RESULT 41

US-09-952-768-2
; Sequence 2, Application US/09952768
; Patent No. US20020035242A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; ; Fernandes-Alnemri, Teresa

; Litwack, Gerald
; Armstrong, Robert
; Tomaselli, Kevin
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING AND METHODS OF USE
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: Suite 6300, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/952,768
; FILING DATE: 10-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 480140.424C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 692-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 479 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-952-768-2

Query Match 2.4%; Score 10; DB 9; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
Db 349 KPCLFFFIQAC 358

RESULT 42

US-09-954-697-33
; Sequence 33, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: THEREOF
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-33

Query Match 2.4%; Score 10; DB 9; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
Db 349 KPCLFFFIQAC 358

RESULT 43

US-09-009-893-4
; Sequence 4, Application US/09009893
; Publication No. US20030087339A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: GENTZ, REINER L.
; APPLICANT: KENNY, JOSEPH J.
; TITLE OF INVENTION: 1-FLICE, A NOVEL INHIBITOR OF TUMOR
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,893
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,205
; FILING DATE: 21-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/054,800
; FILING DATE: 05-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0970002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 479 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-009-893-4

Query Match 2.4%; Score 10; DB 10; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFFIQAC 287
Db 349 KPCLFFFIQAC 358

RESULT 44

US-10-668-955-2
; Sequence 2, Application US/10668955
; Publication No. US20040054148A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,

NUCLEIC ACIDS ENCODING AND METHODS OF USE

NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: Suite 6300, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/668,955
FILING DATE: 22-Sep-2003
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Laherty, Carol D.
REGISTRATION NUMBER: 51,909
REFERENCE/DOCKET NUMBER: 480140.424D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-668-955-2

Query Match 2.4%; Score 10; DB 12; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFFIQAC 287
| | | | | | | | | |
Db 349 KPKLFFFIQAC 358

RESULT 45
US-10-713-208-4
Sequence 4, Application US/10713208
Publication No. US20040121387A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: I-FLICE, A Novel Inhibitor of Tumor Necrosis Factor Receptor-1 and
TITLE OF INVENTION: CD-95 Induced Apoptosis
FILE REFERENCE: PF381C1D1
CURRENT APPLICATION NUMBER: US/10/713,208
CURRENT FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: US 09/489,155
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/009,893
PRIOR FILING DATE: 1998-01-21
PRIOR APPLICATION NUMBER: US 60/054,800
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/034,205
PRIOR FILING DATE: 1997-01-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapiens

Query Match 2.4%; Score 10; DB 16; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFFIQAC 287
| | | | | | | | | |
Db 349 KPKLFFFIQAC 358

RESULT 46
US-09-962-834A-2
Sequence 2, Application US/09962834A
Patent No. US20020034813A1
GENERAL INFORMATION:
APPLICANT: Bowman, Michael
TITLE OF INVENTION: NOVEL PROTEASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,834A
FILING DATE: 25-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 08/675,123
FILING DATE: 1996-07-03
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15276
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 521 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-962-834A-2

Query Match 2.4%; Score 10; DB 9; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPKLFFFIQAC 287
| | | | | | | | | |
Db 392 KPKLFFFIQAC 401

RESULT 47
US-09-851-873-103
Sequence 103, Application US/09851873
Publication No. US20030165488A1
GENERAL INFORMATION:
APPLICANT: Kletzien, Rolf F
APPLICANT: Reardon, Ilene M
APPLICANT: Weiland, Katherine L
TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
FILE REFERENCE: 28341/00233
CURRENT APPLICATION NUMBER: US/09/851,873
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 105
SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 103
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-951-873-103

Query Match 2.4%; Score 10; DB 10; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPXLFFFIQAC 287
Db 392 KPXLFFFIQAC 401
|||||

RESULT 48

US-10-439-676-2
; Sequence 2, Application US/10439676
; Publication No. US20030180935A1
; GENERAL INFORMATION:

; APPLICANT: Bowman, Michael
; TITLE OF INVENTION: NOVEL PROTEASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/439,676

; FILING DATE: 16-May-2003

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/08/675,123

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Brown, Scott A.

; REGISTRATION NUMBER: 32,724

; REFERENCE/DOCKET NUMBER: G15276

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 498-8224

; TELEFAX: (617) 876-5851

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 521 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-439-676-2

Query Match 2.4%; Score 10; DB 14; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPXLFFFIQAC 287
Db 392 KPXLFFFIQAC 401
|||||

RESULT 49

US-09-410-194-21

; Sequence 21, Application US/09410194

; Patent No. US20020095030A1

; GENERAL INFORMATION:

; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmeler, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schroter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean- Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-21

Query Match 2.4%; Score 10; DB 9; Length 571;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPXLFFFIQAC 287
Db 392 KPXLFFFIQAC 401
|||||

RESULT 50

US-09-954-697-56

; Sequence 56, Application US/09954697

; Patent No. US20020106631A1

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSSES

; FILE REFERENCE: 480140.431D2

; CURRENT APPLICATION NUMBER: US/09/954,697

; CURRENT FILING DATE: 2001-09-14

; NUMBER OF SEQ ID NOS: 116

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 56

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-954-697-56

Query Match 2.2%; Score 9; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 FIQACGGEQ 291
Db 1 FIQACGGEQ 9
|||||

Search completed: August 3, 2004, 09:16:26
Job time : 46 secs

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PD 26-NOV-1997.
XX
XX 13-MAY-1997; 97EP-00303397.
XX
XX 20-MAY-1996; 96US-0017949P.
XX
XX 23-MAY-1996; 96US-0020344P.
XX
XX 05-JUN-1996; 96US-0018961P.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI ) UNIV MICHIGAN.
XX
XX Dixit VM, He W, Ruben SM, Kikly KK;
XX
XX WPI; 1998-001790/01.
XX
XX N-PSDB; AAV09401.
XX
XX DNA encoding interleukin-1 beta converting enzyme apoptosis protease-6 -
XX useful to develop products to treat, e.g. viral infection, tumour,
XX Alzheimer's disease, inflammation, osteoporosis and AIDS.
XX
XX Claim 4; Fig 1; 44pp; English.
XX
XX This is a human interleukin-1 beta converting enzyme apoptosis protease-6
XX (ICE LAP-6) polypeptide. The ICE LAP-6 polypeptide and agonists to the
XX polypeptide can be used to induce apoptosis, e.g. as an antiviral or
XX antitumour agent, control embryonic development and tissue homeostasis
XX and the roles of such factors in dysfunction and disease. Antagonists
XX which inhibit the activity of the ICE LAP-6 polypeptide can be used to
XX treat, Alzheimer's or Parkinson's disease, rheumatoid arthritis, septic
XX shock, sepsis, stroke, chronic, acute or central nervous system
XX inflammation, osteoporosis, ischaemia reperfusion injury, cell death
XX associated with cardiovascular disease, polycystic kidney disease,
XX apoptosis of endothelial cells in cardiovascular disease, degenerative
XX liver disease, multiple sclerosis, cerebellar degeneration, ischaemic
XX injury, myocardial infarction, acquired immunodeficiency syndrome (AIDS),
XX myelodysplastic syndrome, aplastic anaemia, male pattern baldness and
XX head injury damage. They can also be used for detection and diagnosis
XX
XX Sequence 416 AA;
XX
Query Match 100.0%; Score 416; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDEADRLRLRCRLRLVEELQVDQLWDLVLSRELFRPHMIEDIQAGSGSRDDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDLVLSRELFRPHMIEDIQAGSGSRDDQARQLII 60
Qy 61 DLETRGSALEPLFTSCLEDTGQDMLASFLRNRAGKLSKPTLENLTPVVLRLPEIRKEV 120
Db 61 DLETRGSALEPLFTSCLEDTGQDMLASFLRNRAGKLSKPTLENLTPVVLRLPEIRKEV 120
Qy 121 LRPEPRVDIGSGGFGDVGALSLRGADLALAYILSMPECGHCLIIINNFCRESGLRTR 180
Db 121 LRPEPRVDIGSGGFGDVGALSLRGADLALAYILSMPECGHCLIIINNFCRESGLRTR 180
Qy 181 TGSNIDCKLRRRSSLHFVVEVKGDLTAKKMWLALLELARQDHGALDCCVWLISHGQC 240
Db 181 TGSNIDCKLRRRSSLHFVVEVKGDLTAKKMWLALLELARQDHGALDCCVWLISHGQC 240
Qy 241 ASHLQFPQAVYGTGCPVSVKIVNIENGTSKPSLGGKPKLFFTOACGGEOKDHGEFVAS 300
Db 241 ASHLQFPQAVYGTGCPVSVKIVNIENGTSKPSLGGKPKLFFTOACGGEOKDHGEFVAS 300
Qy 301 TSPDESPGSPNEPDATPFQGLRFTFDQLDAISSLPTSPDIFVSYSTPFGVSWRDPKSG 360
Db 301 TSPDESPGSPNEPDATPFQGLRFTFDQLDAISSLPTSPDIFVSYSTPFGVSWRDPKSG 360
Qy 361 SWYVETLDDIFEQWHAHSEDQLSLLLRVANAVSVKGIYKQMPCCNFRLKKLFFKTS 416
Db 361 SWYVETLDDIFEQWHAHSEDQLSLLLRVANAVSVKGIYKQMPCCNFRLKKLFFKTS 416

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RESULT 2

```

AAE00606
ID AAE00606 standard; protein; 416 AA.
XX
XX AAE00606;
XX
XX 02-JUL-2001 (first entry)
XX
XX Human caspase-9, alternative version.
XX
XX Human; caspase-9; interleukin-1 converting enzyme; ICE-LAP6; Mch6;
XX cysteine protease; apoptosis; caspase expression cassette; metastasis;
XX tumour; cathepsin B; urokinase; proliferation; gene therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 28
XX /note= "Encoded by GCC; Ala is present in the sequence
XX shown in page 105-107 (AAE00620)"
XX
XX Misc-difference 96
XX /note= "Encoded by GCA; Ala is present in the sequence
XX shown in page 105-107 (AAE00620)"
XX
XX Misc-difference 139..290
XX /note= "Encoded by GTCGAG; Amino acid residues from
XX position 140 to 289 present in this sequence are not
XX found in the sequence shown in page 105-107 (AAE00620)"
XX
XX Cleavage-site 315..316
XX /label= Proteolytic_cleavage_site
XX
XX Cleavage-site 330..331
XX /label= Proteolytic_cleavage_site
XX
XX WO200129232-A2.
XX
XX 26-APR-2001.
XX
XX 19-OCT-2000; 2000WO-US028941.
XX
XX 20-OCT-1999; 99US-0160559P.
XX
XX 14-AUG-2000; 2000US-0225564P.
XX
XX (SCIO-) SCIOS INC.
XX
XX Cordell B, Li Y;
XX
XX WPI; 2001-290920/30.
XX
XX N-PSDB; AAD03916.
XX
XX Novel fusion polypeptide comprising first and second caspase subunit
XX separated by cleavage site not associated in nature with caspase subunit,
XX useful for cloning gene encoding enzymes involved in proteolytic
XX cleavage.
XX
XX Claim 4; Fig 18; 116pp; English.
XX
XX The present sequence is an alternative version of human Caspase-9 also
XX known as interleukin-1 converting enzyme (ICE) LAP6 and Mch6. Caspases
XX are a family of cysteine proteases, that participate in the initiation
XX and execution of apoptosis. Caspases exist as pro-enzymes, activated by
XX cleavage into a large and small subunit, occurring after specific
XX aspartic acid residues within the pro-enzyme sequence. The present
XX invention relates to a method for functional cloning of genes encoding
XX proteins or enzymes involved in proteolytic cleavage. The invention is
XX based on the use of caspase expression cassettes comprising the coding
XX sequence of a proteolytic cleavage site flanked by sequences encoding two
XX caspase subunits. A fusion polypeptide comprising a first and a second
XX caspase subunit, separated by a cleavage site not associated in nature,
XX is useful for cloning gene encoding enzymes involved in proteolytic
XX cleavage. An expression cassette containing fusion polypeptide is used to
XX identify a mutant cell line deficient in an enzyme of interest and is
XX also useful for diagnosis and suppression of proliferation or metastases
XX of a tumour cell characterised by overexpression of a polypeptide (e.g.

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```
CC Cathepsin B or urokinase, selectively expressed in the tumour cells). DNA
CC encoding fusion polypeptide is used in gene therapy. Note: This sequence
CC SEQ.ID.NO.18 is stated as being the same as that shown in page 105-107
CC (See AAB00620) in the specification. However these sequences differ at
CC several positions
XX
XX Sequence 416 AA;
SQ
Query Match 100.0%; Score 416; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDEADRLRRCKRLRVELOWDQLWDVLLSRELFRPHMEDIQAGSGSRDDQARQLII 60
Db 1 MDEADRLRRCKRLRVELOWDQLWDVLLSRELFRPHMEDIQAGSGSRDDQARQLII 60
QY 61 DLETGSGQALPLFISCLEDTGDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETGSGQALPLFISCLEDTGDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 121 LRPETPRVDIGSGGPDVGALESIRGNADLAYILSMPCGHCLIIINNVNFCRESGLRTR 180
Db 121 LRPETPRVDIGSGGPDVGALESIRGNADLAYILSMPCGHCLIIINNVNFCRESGLRTR 180
QY 181 TGSNDCEKLRREFSLHVEVKGDLTAKKMWLALLELARQDHGALDCCVVILSHGCG 240
Db 181 TGSNDCEKLRREFSLHVEVKGDLTAKKMWLALLELARQDHGALDCCVVILSHGCG 240
QY 241 ASHLOPPGAVYGTGCPVSVKEIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFVEVAS 300
Db 241 ASHLOPPGAVYGTGCPVSVKEIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFVEVAS 300
QY 301 TSPEDSPGSGNPEPDATPQEGRLTFDQLDAISSLTPSDIFVSYSTFPFGVSWRDPKSG 360
Db 301 TSPEDSPGSGNPEPDATPQEGRLTFDQLDAISSLTPSDIFVSYSTFPFGVSWRDPKSG 360
QY 361 SWVETLDDIFEQWAHSEDLSILLRVANAVSVKGIYKOMPFCNFKLKFKTS 416
Db 361 SWVETLDDIFEQWAHSEDLSILLRVANAVSVKGIYKOMPFCNFKLKFKTS 416
RESULT 3
ID AAY21723 standard; protein; 416 AA.
AC AAY21723;
XX
XX 10-SEP-1999 (first entry)
XX
XX Amino acid sequence of caspase-9 (ICE-LAP6).
XX
XX Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
XX autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
XX tumour cell; myocardial infarction; human.
XX
XX Homo sapiens.
XX
XX WO9935277-A2.
XX
XX 15-JUL-1999.
XX
XX 11-JAN-1999; 99WO-US000632.
XX
XX 09-JAN-1998; 98US-0070987P.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 1999-419353/35.
XX
XX N-PSDB; AAX81225.
XX
XX New isolated nucleic acid molecule encoding a rev-caspase - used for
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PT screening and identifying inhibitors or enhancers for treating cancer or
PT autoimmune disease.
XX
XX Disclosure; Fig 19A-B; 7app; English.
XX
XX The invention relates to nucleic acid molecules encoding rev-caspases.
XX Rev-caspases are cysteine proteases that specifically cleave proteins.
XX Asp residues and is expressed as a zymogen, in which the small
XX subunit is N-terminal to a large subunit. A gene delivery vehicle
XX comprising a rev-caspase coding sequence is useful for the treatment of
XX cancer, where the gene delivery vehicle is internalised by tumour cells.
XX The gene delivery vehicle can also be used to treat autoimmune diseases.
XX Cells transfected with a rev-caspase expressing vector can be used in
XX identification of inhibitors or enhancers of caspase-mediated apoptosis.
XX In vitro translated rev-caspase can be used to identify an inhibitor or
XX enhancer of caspase processing activity. Caspase inhibitors are useful
XX for treating neurodegenerative diseases as well as for inhibiting
XX apoptosis in the heart following myocardial infarction. Sequences
XX AAX81217 -AAX81226 represent human caspase genes encoding caspase 1-10
XX gene products (AAY21715-Y21724)
XX
XX Sequence 416 AA;
SQ
Query Match 52.6%; Score 219; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 2.3e-208;
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 198 HFMVVKGDLTAKKMWLALLELARQDHGALDCCVVILSHGCOASHLOPPGAVYGTGCP 257
Db 198 HFMVVKGDLTAKKMWLALLELARQDHGALDCCVVILSHGCOASHLOPPGAVYGTGCP 257
QY 258 VSVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFVEVASTPDESPGSGNPEPDAT 317
Db 258 VSVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFVEVASTPDESPGSGNPEPDAT 317
QY 318 PQEGLRTPDQLDAISSLTPSDIFVSYSTFPFGVSWRDPKSGVYVETLDDIFEQWAHS 377
Db 318 PQEGLRTPDQLDAISSLTPSDIFVSYSTFPFGVSWRDPKSGVYVETLDDIFEQWAHS 377
QY 378 EDLQSLLLRVANAVSVKGIYKOMPFCNFKLKFKTS 416
Db 378 EDLQSLLLRVANAVSVKGIYKOMPFCNFKLKFKTS 416
RESULT 4
ABJ01224
ID ABJ01224 standard; protein; 416 AA.
XX
XX AC ABJ01224;
XX
XX 18-SEP-2002 (first entry)
XX
XX Human caspase-9 SEQ ID NO: 30.
XX
XX Human; caspase; rev-caspase; gene therapy; protease; apoptosis; cancer;
XX autoimmune disease; cytostatic; immunosuppressive.
XX
XX Homo sapiens.
XX
XX US6376226-B1.
XX
XX 23-APR-2002.
XX
XX 26-APR-2000; 2000US-00561756.
XX
XX 09-JAN-1998; 98US-0070897P.
XX
XX 08-JAN-1999; 99US-00227721.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 2002-453146/48.
XX
```

DR N-PSDB; ABT03972.
 XX New rev-caspases engineered to contain the small subunit fused in frame N
 PT -terminal to the large subunit, which is in reverse order to the wild
 PT type caspases, are useful to treat cancer and autoimmune diseases.
 XX
 PS Disclosure; Fig 19; 81pp; English.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences
 CC can be used in the gene therapy of cancer and autoimmune diseases. The
 CC present sequence is a protein described in the exemplification of the
 CC invention
 XX
 SQ Sequence 416 AA;
 Query Match 52.6%; Score 219; DB 5; Length 416;
 Best Local Similarity 100.0%; Pred. No. 2.3e-208;
 Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 198 HFMEVKGDLTAKWVLALELARODRGALDCCVVILSHGCCQASHLQFPQAVYGTGCP 257
 Db 198 HFMEVKGDLTAKWVLALELARODRGALDCCVVILSHGCCQASHLQFPQAVYGTGCP 257
 QY 258 VSVEKIVNIENGTSCLPGKPKLFFIQACGGEQKHGFVASTSPDESPGNSPEPDAT 317
 Db 258 VSVEKIVNIENGTSCLPGKPKLFFIQACGGEQKHGFVASTSPDESPGNSPEPDAT 317
 QY 318 PFQEGRLTFQDLAISLPTSPDIFVSYSYTFPGFVSWRDPKSGSWYVETLDDIFEQWAHS 377
 Db 318 PFQEGRLTFQDLAISLPTSPDIFVSYSYTFPGFVSWRDPKSGSWYVETLDDIFEQWAHS 377
 QY 378 EDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
 Db 378 EDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 5
 ADA10646
 ID ADA10646 standard; protein; 416 AA.

XX ADA10646;
 XX AC
 XX 06-NOV-2003 (first entry)
 XX Human caspase-9 protein.
 XX Human; caspase-9; anti-HIV; neurotropic; neuroprotective; vasotropic;
 KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease.
 XX
 OS Homo sapiens.
 XX US2002160975-A1.
 XX 31-OCT-2002.
 XX 06-FEB-2002; 2002US-00068569.
 XX 08-FEB-2001; 2001US-0267966P.
 XX 24-AUG-2001; 2001US-00939293.
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX Alnemri ES;
 XX WPI; 2003-219992/21.
 XX N-PSDB; ADA10661.
 XX New nucleic acid molecules encoding a peptide or polypeptide that binds
 PT to a portion of an inhibitor of apoptosis protein, useful for inducing

PT apoptosis and identifying inhibitors or enhancers of apoptosis for
 PT treating AIDS, or cancer.
 XX Claim 36; Page 25-26; 52pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule comprising a
 CC polynucleotide that encodes a polypeptide or peptide, or its variants
 CC that specifically binds to at least a portion of an inhibitor of
 CC apoptosis protein (IAP). Also included are a peptide or a polypeptide
 CC (comprising at least an N terminus sequence of caspase-9 N-terminal
 CC linker sequence, a first portion of a procaspase-9 that specifically
 CC binds at least a portion of an IAP and a second portion of a procaspase-9
 CC containing a mutated active site, where the peptide or polypeptide
 CC specifically binds at least a portion of an IAP and lacks cysteine
 CC protease activity, and at least a portion of caspase-3, where the peptide
 CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
 CC an IAP or an IAP Bir3 domain) or at least a portion of a mutated
 CC procaspase-9, which fails to undergo normal processing and possesses wild
 CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
 CC polynucleotide sequence that encodes the caspase-9 N-terminal linker), an
 CC expression vector comprising any of the nucleic acids, a host cell
 CC containing the expression vector, an antibody that specifically binds to
 CC the peptide or polypeptide, an antibody that specifically binds to an
 CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
 CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
 CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
 CC identifying a compound that inhibits the peptide or polypeptide,
 CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
 CC a process for the manufacture of a compound for inhibiting or enhancing
 CC apoptosis in a cell. The nucleic acid molecules and peptides or
 CC polypeptides are useful for inducing apoptosis and identifying inhibitors
 CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
 CC ischaemic injury, cancer, autoimmune diseases. The present sequence
 CC represents the full length caspase-9 protein.
 XX
 SQ Sequence 416 AA;

Query Match 52.6%; Score 219; DB 6; Length 416;
 Best Local Similarity 99.7%; Pred. No. 2.3e-208;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 97 KLSKPTLENTPVVLRPEIRKPEVLRPETPRPDVIGSGFGDVGALESIRGNADLAYILS 156
 Db 97 KLSKPTLENTPVVLRPEIRKPEVLRPETPRPDVIGSGFGDVGALESIRGNADLAYILS 156
 QY 157 MEPGCHLIINNVNFCRESGLRRTGSDICEKLRRFSSLHFVVEVKGDLTAKWVLA 216
 Db 157 MEPGCHLIINNVNFCRESGLRRTGSDICEKLRRFSSLHFVVEVKGDLTAKWVLA 216
 QY 217 LELARQDHGALDCCVVVILSHGCCQASHLQFPQAVYGTGCPVSVKEKIVNIENGTSCLPG 276
 Db 217 LELARQDHGALDCCVVVILSHGCCQASHLQFPQAVYGTGCPVSVKEKIVNIENGTSCLPG 276
 QY 277 GKPKLFFIQACGGEQKHGFVASTSPDESPGNSPEPDATPPQEGRLTFQDLAISL 336
 Db 277 GKPKLFFIQACGGEQKHGFVASTSPDESPGNSPEPDATPPQEGRLTFQDLAISL 336
 QY 337 TPSDIFVSYSYTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGI 396
 Db 337 TPSDIFVSYSYTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGI 396
 QY 397 YKQMPGCFNLRKLLFFKTS 416
 Db 397 YKQMPGCFNLRKLLFFKTS 416

RESULT 6
 AA39208
 ID AA39208 standard; peptide; 203 AA.
 XX
 AC AA39208;
 XX 18-MAY-1998 (first entry)
 DT

```
XX DE Human ICE LAP-6 amino acid sequence variant.
XX KW ICE LAP-6; interleukin-1 beta converting enzyme apoptosis protease-6;
XX KW viral infection; tumour; inflammation; osteoporosis; AIDS; human;
XX KW Alzheimer's disease; variant.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 203
FT FT /note= "encoded by TAA"
XX EP080904-A2.
XX PD 26-NOV-1997.
XX PF 19-MAY-1997; 97EP-00303397.
XX PR 20-MAY-1996; 96US-0017949P.
XX PR 23-MAY-1996; 96US-0020344P.
XX PR 05-JUN-1996; 96US-0018961P.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (UNMI ) UNIV MICHIGAN.
XX PI Dixit VM, He W, Ruben SM, Kikly KK;
XX WPI; 1998-001790/01.
XX N-PSDB; AAV09402.
XX DNA encoding interleukin-1 beta converting enzyme apoptosis protease-6 -
XX useful to develop products to treat, e.g. viral infection, tumour,
XX Alzheimer's disease, inflammation, osteoporosis and AIDS.
XX Disclosure; Fig 5; 44pp; English.
XX This is an amino acid sequence variant of human interleukin-1 beta
XX converting enzyme apoptosis protease-6 (ICE LAP-6) polypeptide. The ICE
XX LAP-6 polypeptide and agonists to the polypeptide can be used to induce
XX apoptosis, e.g. as an antiviral or antitumour agent, control embryonic
XX development and tissue homeostasis and the roles of such factors in
XX dysfunction and disease. Antagonists which inhibit the activity of the
XX ICE LAP-6 polypeptide can be used to treat, Alzheimer's or Parkinson's
XX disease, rheumatoid arthritis, septic shock, sepsis, stroke, chronic,
XX acute or central nervous system inflammation, osteoporosis, ischaemia
XX reperfusion injury, cell death associated with cardiovascular disease,
XX polycystic kidney disease, apoptosis of endothelial cells in
XX cardiovascular disease, degenerative liver disease, multiple sclerosis,
XX cerebellar degeneration, ischaemic injury, myocardial infarction,
XX acquired immunodeficiency syndrome (AIDS), myelodysplastic syndrome,
XX aplastic anaemia, male pattern baldness and head injury damage. They can
XX also be used for detection and diagnosis
XX Sequence 203 AA;
XX Query Match 48.6%; Score 202; DB 2; Length 203;
XX Best Local Similarity 100.0%; Pred. NO. 9.1e-192;
XX Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 212 MVLALLELARQDHGALDCCVWVILSHGCOASHLPFGAVYGTGCPVSEKIVNIFNGTS 271
XX 1 MVLALLELARQDHGALDCCVWVILSHGCOASHLPFGAVYGTGCPVSEKIVNIFNGTS 60
XX 272 CPSLGGKPLFTIQAGGQKDHGEVASTSPEDSPGNSNPEDATPQEGRLTQDQDA 331
XX 61 CPSLGGKPLFTIQAGGQKDHGEVASTSPEDSPGNSNPEDATPQEGRLTQDQDA 120
XX 332 ISSLPTSPDIFVSYSTFFPGFVSWRDPFKSGSVYVETLDDIFEQWAHSEDIQSLLLRVANAV 391
XX 121 ISSLPTSPDIFVSYSTFFPGFVSWRDPFKSGSVYVETLDDIFEQWAHSEDIQSLLLRVANAV 180
```

```
QY 392 SVKGIYKQMPGCFNFKKLPF 413
Db 181 SVKGIYKQMPGCFNFKKLPF 202
RESULT 7
AAG67375
ID AAG67375 standard; protein; 416 AA.
XX AC AAG67375;
XX DT 13-NOV-2001 (first entry)
XX DE Amino acid sequence of human Mch6 polypeptide.
XX Mch6; ced-3 homologue; ICE; interleukin-1-beta converting enzyme;
XX aspartate-specific cysteine protease; ASCP; apoptotic cell death;
XX Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
XX retinitis pigmentosa; cerebellar degeneration; myelodysplastic syndrome;
XX aplastic anemia; ischemic injury; myocardial infarction; stroke; cancer;
XX reperfusion injury; autoimmune disease; systemic lupus erythematosus;
XX immune-mediated glomerulonephritis; viral infection; cell death.
XX OS Homo sapiens.
XX PN US6274318-B1.
XX PD 14-AUG-2001.
XX PF 13-MAY-1999; 99US-00311760.
XX PR 29-MAY-1997; 97US-00865579.
XX PA (UYJE-) UNIV JEFFERSON THOMAS.
XX PI Alnemri ES, Fernandes-Alnemri T, Litwack G;
XX WPI; 2001-540372/60.
XX N-PSDB; AAH77927.
XX Identifying mammalian homologue ced-3 homolog (Mch)6 activity modulators,
XX useful for treating lymphomas, carcinomas and hormone dependent tumors,
XX Alzheimer's disease, Parkinson's disease, comprises using Mch6
XX polypeptide.
XX Example 1; Fig 1a-c; 36pp; English.
XX The present sequence represents a human Mch6 polypeptide. Mch6 is a ced-3
XX homologue, and is a member of the ICE (interleukin-1-beta converting
XX enzyme) family of aspartate-specific cysteine proteases (ASCPs). The
XX specification describes a method for identifying mammalian Mch6 activity
XX modulators (inhibitors or enhancers). The compounds identified by the
XX method are useful as pharmaceuticals for treating or preventing diseases
XX characterized by increased apoptotic cell death such as Alzheimer's
XX disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis
XX pigmentosa, or cerebellar degeneration, myelodysplastic syndromes such as
XX aplastic anemia, ischemic injury including myocardial infarction, stroke
XX and reperfusion injury. The compounds are also useful for treating
XX diseases characterized by loss of apoptotic cell death such as cancers,
XX e.g. lymphomas, carcinomas and hormone dependent tumours such as breast,
XX prostate and ovarian cancer. Increased cell survival or apoptosis
XX inhibition also results in autoimmune diseases such as systemic lupus
XX erythematosus and immune-mediated glomerulonephritis as well as viral
XX infections such as herpes virus, pox virus and adenovirus and the novel
XX identified compounds are useful for treating these conditions. The Mch6
XX inhibitors are used to treat or to reduce severity of diseases
XX characterized by increased programmed cell death
XX Sequence 416 AA;
XX Query Match 46.9%; Score 195; DB 4; Length 416;
XX Best Local Similarity 100.0%; Pred. NO. 1.5e-184;
XX Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 222 QDHGALDCCVVWILSHGCQASHLOFPQAVYGTGCPVSVKEKVINFGTSCPSLGGKPKL 281
 Db 222 QDHGALDCCVVWILSHGCQASHLOFPQAVYGTGCPVSVKEKVINFGTSCPSLGGKPKL 281
 QY 282 FFIQACGGEQKDHGFVASTSPEDSPGNSPEPDATPFQGLRTFDQDLAISLPTPSDI 341
 Db 282 FFIQACGGEQKDHGFVASTSPEDSPGNSPEPDATPFQGLRTFDQDLAISLPTPSDI 341
 QY 342 FVSYSTPPGFSVRDPSKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
 Db 342 FVSYSTPPGFSVRDPSKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
 QY 402 GCFNFKLKKLFFKTS 416
 Db 402 GCFNFKLKKLFFKTS 416

RESULT 8
 AAU08315
 ID AAU08315 standard; protein; 416 AA.
 XX AAU08315;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 XX Human aspartate-specific cysteine protease, MCH6.
 XX
 XX Human; aspartate-specific cysteine protease; MCH6; neurotropic;
 KW neuroprotective; anti-Parkinsonian; antianaemic; vasotropic; cardiant;
 KW cerebroprotective; mammalian ced-3 homologue 6; gene therapy; apoptosis;
 KW Alzheimer's disease; Parkinson's disease; retinitis pigmentosa;
 KW cerebellar degeneration; myelodysplastic syndrome; aplastic anaemia;
 KW ischaemic injury; myocardial infarction; stroke; reperfusion injury;
 KW amyotrophic lateral sclerosis.
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Active-site 285..289
 FT Cleavage-site 312..316
 FT /label= Granzyme beta_cleavage site
 FT /note= "Cleavage occurs after Asp at position 315"
 FT Cleavage-site 327..331
 FT /label= Granzyme beta_cleavage site
 FT /note= "Cleavage occurs after Asp at position 330"
 XX
 PN US2001016345-A1.
 XX
 XX 23-AUG-2001.
 XX
 XX 22-DEC-2000; 2000US-00746731.
 PF
 XX 29-MAY-1997; 97US-00865579.
 PR
 XX 25-FEB-1999; 99US-00257218.
 XX
 XX (ALNE/) ALNEMRI E S.
 PA (PERN/) FERNANDES-ALNEMRI T.
 PA (LITW/) LITWACK G.
 XX
 XX Alnemri ES, Fernandes-Alnemri T, Litwack G;
 XX WPI; 2001-535542/59.
 DR N-PSDB; AAS12629.
 XX
 XX New Mch6 polypeptides and genes encoding the polypeptides useful for
 PT diagnosing, treating or reducing the severity of cell death-mediated
 PT diseases such as neurodegenerative diseases e.g. Alzheimer's disease,
 PT Parkinson's disease.
 XX
 XX Claim 8; Fig 1; 15pp; English.
 PS
 XX The invention relates to an isolated gene encoding MCH6 (mammalian ced-3

CC homologue 6) an aspartate-specific cysteine protease and the MCH6
 CC polypeptide. The MCH6-encoding nucleic acids and polypeptides can be used
 CC to diagnose, treat (e.g. by gene therapy) or reduce the severity of cell
 CC death-mediated diseases (i.e. apoptotic) such as neurodegenerative
 CC diseases e.g. Alzheimer's disease, Parkinson's disease, amyotrophic
 CC lateral sclerosis, retinitis pigmentosa and cerebellar degeneration, and
 CC myelodysplastic syndromes, e.g. aplastic anaemia, ischaemic injury,
 CC myocardial infarction, stroke and reperfusion injury. The MCH6-encoding
 CC nucleic acids and polypeptides can also be used to diagnose or generate
 CC reagents to diagnose diseases mediated or characterised by programmed
 CC cell death. A purified recombinant MCH6 protein can be used to measure
 CC hydrolysis rates for various substrates such as DEVD-AMC and YVAD-AMC in
 CC a continuous fluorometric assay. The present sequence represents human
 CC MCH6

XX Sequence 416 AA;

Query Match 46.9%; Score 195; DB 4; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.5e-184;
 Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 QDHGALDCCVVWILSHGCQASHLOFPQAVYGTGCPVSVKEKVINFGTSCPSLGGKPKL 281
 Db 222 QDHGALDCCVVWILSHGCQASHLOFPQAVYGTGCPVSVKEKVINFGTSCPSLGGKPKL 281
 QY 282 FFIQACGGEQKDHGFVASTSPEDSPGNSPEPDATPFQGLRTFDQDLAISLPTPSDI 341
 Db 282 FFIQACGGEQKDHGFVASTSPEDSPGNSPEPDATPFQGLRTFDQDLAISLPTPSDI 341
 QY 342 FVSYSTPPGFSVRDPSKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
 Db 342 FVSYSTPPGFSVRDPSKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
 QY 402 GCFNFKLKKLFFKTS 416
 Db 402 GCFNFKLKKLFFKTS 416

RESULT 9
 AAE08938
 ID AAE08938 standard; protein; 416 AA.
 XX
 AC AAE08938;
 XX
 XX 15-NOV-2001 (first entry)
 DT
 XX Mammalian ced-3 homologue 6 (Mch6).
 DE
 XX
 XX Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer;
 KW aspartate-specific cysteine protease; ASCP; apoptosis; therapy;
 KW autoimmune disease; cerebellar degeneration; Alzheimer's disease;
 KW cytostatic; Parkinson's disease; immunomodulator; antimicrobial;
 KW viral infection; cell death-mediated disease; neuroprotective.
 XX
 OS Unidentified.

XX
 XX Key Location/Qualifiers
 FH
 FT Active-site 285..290
 FT /note= "Active site pentapeptide"
 FT Cleavage-site 315..316
 FT Cleavage-site 330..331
 XX
 XX US6271361-B1.
 PN
 XX
 XX 07-AUG-2001.
 PD
 XX 25-FEB-1999; 99US-00257218.
 PF
 XX 29-MAY-1997; 97US-00865579.
 PR
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 PA
 XX Alnemri ES, Fernandes-Alnemri T, Litwack G;

XX WPI; 2001-528686/58.
 DR N-PSDB; AAD15656.
 XX
 PT New apoptotic genes and their apoptotic protease products, useful for
 PT modulating apoptosis for the therapeutic treatment of human diseases,
 PT e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's
 PT disease.
 XX
 PS Claim 2; Fig 1; 36pp; English.
 XX
 CC The invention relates to an isolated gene encoding apoptotic protease,
 CC mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the aspartate-
 CC specific cysteine protease (ASCP) family. Mch6 DNA and protein sequences
 CC are useful for modulating apoptosis for the therapeutic treatment of
 CC human diseases. Mch6 sequences are useful for upregulating apoptosis
 CC (e.g. for treating cancers, autoimmune disease or viral infections) or
 CC downregulating apoptosis (e.g. for treating Alzheimer's disease,
 CC Parkinson's disease or cerebellar degeneration). The Mch6 sequence is
 CC useful for diagnosing, treating or reducing the severity of cell death-
 CC mediated diseases, as well as other diseases mediated by either increased
 CC or decreased programmed cell death. The present amino acid sequence is
 CC Mch6
 XX
 SQ Sequence 416 AA;
 Query Match 46.9%; Score 195; DB 4; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.5e-184;
 Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 222 QDHGALDCCVWVILSHGCOASHLQFPAGVYGTGCPVSVKEIVNIFNGTSCPSLGGKPKL 281
 DB 222 QDHGALDCCVWVILSHGCOASHLQFPAGVYGTGCPVSVKEIVNIFNGTSCPSLGGKPKL 281
 QY 282 FFIQACGGEQKHGFEVASTSPEDSPGNSNPEDATPFQEGRLTFDQLDAISLPTPSDI 341
 DB 282 FFIQACGGEQKHGFEVASTSPEDSPGNSNPEDATPFQEGRLTFDQLDAISLPTPSDI 341
 QY 342 FVSYSTFFGFSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKOMP 401
 DB 342 FVSYSTFFGFSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKOMP 401
 QY 402 GCFNLRKKLFFKTS 416
 DB 402 GCFNLRKKLFFKTS 416
 RESULT 10
 AAB84374
 ID AAB84374 standard; protein; 416 AA.
 AC AAB84374;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 DE Amino acid sequence of aspartate-specific cysteine protease Mch6.
 XX
 KW Human; apoptotic protease; Mch6; aspartate-specific cysteine protease;
 KW cell death; cancer; autoimmune disease; systemic lupus erythematosus;
 KW viral infection; degenerative disorder; Alzheimer's disease;
 KW Parkinson's disease; myelodysplastic syndrome; myocardial infarction;
 KW stroke.
 XX
 OS Homo sapiens.
 XX
 PN US2001006779-A1.
 XX
 PD 05-JUL-2001.
 XX
 PF 29-MAY-1997; 97US-00865579.
 XX
 PR 29-MAY-1997; 97US-00865579.
 XX

PA (ALNE/) ALNEMRI E S.
 PA (FERN/) FERNANDES-ALNEMRI T.
 PA (LITW/) LITWACK G.
 XX
 PI Alnemri ES, Fernandes-Alnemri T, Litwack G;
 XX
 DR WPI; 2001-389294/41.
 DR N-PSDB; AAH25191.
 XX
 PT Isolated gene encoding a human apoptotic protease known as Mch6, useful
 PT in the diagnosis or treatment of cell death-mediated conditions, e.g.
 PT cancers and autoimmune diseases such as systemic lupus erythematosus.
 XX
 PS Claim 8; Fig 1A-C; 15pp; English.
 XX
 CC The present sequence represents a human apoptotic protease, designated
 CC Mch6. Mch6 is an aspartate-specific cysteine protease. Mch6 polypeptides
 CC and polynucleotides can be used to diagnose, treat or reduce the severity
 CC of cell death-mediated conditions, e.g. cancers, autoimmune diseases such
 CC as systemic lupus erythematosus, viral infections such as herpesvirus,
 CC degenerative disorders such as Alzheimer's disease and Parkinson's
 CC disease, myelodysplastic syndromes such as myocardial infarction and
 CC stroke. They can also be used to screen for compounds that inhibit or
 CC promote Mch6 mediated apoptosis
 XX
 SQ Sequence 416 AA;
 Query Match 46.9%; Score 195; DB 4; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.5e-184;
 Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 222 QDHGALDCCVWVILSHGCOASHLQFPAGVYGTGCPVSVKEIVNIFNGTSCPSLGGKPKL 281
 DB 222 QDHGALDCCVWVILSHGCOASHLQFPAGVYGTGCPVSVKEIVNIFNGTSCPSLGGKPKL 281
 QY 282 FFIQACGGEQKHGFEVASTSPEDSPGNSNPEDATPFQEGRLTFDQLDAISLPTPSDI 341
 DB 282 FFIQACGGEQKHGFEVASTSPEDSPGNSNPEDATPFQEGRLTFDQLDAISLPTPSDI 341
 QY 342 FVSYSTFFGFSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKOMP 401
 DB 342 FVSYSTFFGFSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKOMP 401
 QY 402 GCFNLRKKLFFKTS 416
 DB 402 GCFNLRKKLFFKTS 416
 RESULT 11
 ABB82738
 ID ABB82738 standard; protein; 416 AA.
 AC ABB82738;
 XX
 DT 07-MAR-2003 (first entry)
 XX
 DE Human caspase-9 polypeptide.
 XX
 KW Caspase-9; TUCAN; cancer; biomarker; cIAP2; Apaf1; Bcl-2; Smac; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200290931-A2.
 XX
 PD 14-NOV-2002.
 XX
 PF 07-MAY-2002; 2002WO-US014487.
 XX
 PR 07-MAY-2001; 2001US-0289223P.
 PR 12-FEB-2002; 2002US-0356934P.
 XX
 PA (BURN-) BURNHAM INST.
 XX

PI Reed JC;
 XX WPI; 2003-111999/10.
 XX
 PT Determining a prognosis for survival for a cancer patient, useful for
 PT determining if the patient is at risk for relapse, comprises measuring a
 PT level of TUCAN in a sample from the patient, and comparing it to a
 PT reference level.
 XX
 XX Example; Page 125-126; 153pp; English.
 XX
 CC The invention relates to determining a prognosis for survival for a
 CC cancer patient. The method involves (a) measuring a level of a tumour up-
 CC regulated CARD-containing antagonist of caspase-9 (TUCAN) in a neoplastic
 CC cell-containing sample from the cancer patient; and (b) comparing the
 CC level of TUCAN in the sample to a reference level of TUCAN, where a low
 CC level of TUCAN in the sample correlates with increased survival of the
 CC patient. Alternatively, the method involves measuring levels of TUCAN and
 CC one or more biomarkers selected from the group of cIAP2, Apaf1, Bcl-2, or
 CC Snac in a neoplastic cell-containing sample from the cancer patient. The
 CC method is useful for determining if the patient is at risk for relapse,
 CC or for determining a proper course of treatment for a patient with
 CC cancer. The method is also useful for monitoring the effectiveness of a
 CC course of treatment for a patient with cancer, e.g. colon cancer,
 CC gastrointestinal cancer, breast cancer, ovarian cancer, lung cancer,
 CC leukemia, CNS cancer, melanoma, prostate cancer, or renal cancer. The
 CC present sequence represents a human caspase-9 polypeptide
 XX
 SQ Sequence 416 AA;
 Query Match 46.9%; Score 195; DB 6; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.5e-184;
 Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 222 QDHGALDCCVVVILSHGQASHLQFPGAVYGTGCPVSVKIVNIFNGTSCPSLGKPKL 281
 Db 222 QDHGALDCCVVVILSHGQASHLQFPGAVYGTGCPVSVKIVNIFNGTSCPSLGKPKL 281
 QY 282 FFIQACGGEQKHGFVASTSPEDSPGNSPEPDATPFQGLRTFDQLDAISSLTSPSDI 341
 Db 282 FFIQACGGEQKHGFVASTSPEDSPGNSPEPDATPFQGLRTFDQLDAISSLTSPSDI 341
 QY 342 FVSYSTPPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
 Db 342 FVSYSTPPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
 QY 402 GCNFKLKKLFFKTS 416
 Db 402 GCNFKLKKLFFKTS 416
 RESULT 12
 ADE52020
 ID ADE52020 standard; protein; 416 AA.
 AC ADE52020;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 DE Human mammalian ced-3 homologue 6 (Mch6).
 KW cytostatic; virucide; nontropic; neuroprotective; antiparkinsonian;
 KW cardiant; apoptosis modulator; aspartate-specific cysteine protease;
 KW gene therapy; aspartate-specific cysteine protease agonist;
 KW aspartate-specific cysteine protease antagonist; Mch6;
 KW mammalian ced-3 homologue 6; apoptosis; cancer; viral infection;
 KW degenerative disorder; Alzheimers disease; Parkinsons disease;
 KW myocardial infarction; human; mammalian ced-3 homologue 6; Mch6.
 XX Homo sapiens.
 OS
 XX US2002189504-A1.
 FN
 XX

PD 05-DEC-2002.
 XX 29-JAN-2002; 2002US-00059749.
 XX
 XX 29-MAY-1997; 97US-00865579.
 PR 25-FEB-1999; 99US-00257218.
 PR 22-DEC-2000; 2000US-00746731.
 XX
 PA (UYJB-) UNIV JEFFERSON THOMAS.
 XX
 XX Alnemri ES, Fernandes-Alnemri T, Litwack G;
 PI WPI; 2004-040943/04.
 XX
 DR New isolated gene encoding a mammalian ced-3 homolog 6, for modulating
 XX apoptosis for the therapeutic treatment of human diseases, such as
 PT cancers and degenerative disorders.
 PT
 PT Claim 8; SEQ ID NO 2; 15pp; English.
 PS
 XX The invention describes an isolated gene (I) encoding Mch6 (mammalian ced
 CC -3 homologue 6), or a functional fragment of it. (I) And the polypeptide
 CC encoded by (I) is used to modulate apoptosis for the therapeutic
 CC treatment of human diseases. (I) Is used to prepared a recombinant
 CC aspartate-specific cysteine protease, that it encodes. The recombinant
 CC protease can be used to screen for Mch6 inhibitors. Disorders involving
 CC apoptosis that can be diagnosed or treated by (I) or the polypeptide it
 CC encodes, including cancers, viral infections, degenerative disorders,
 CC such as Alzheimers and Parkinsons disease, and myocardial infarction.
 CC This is the amino acid sequence of human mammalian ced-3 homologue 6
 CC (Mch6), a member of the aspartate-specific cysteine protease (ASCP)
 CC family of proteases.
 XX
 XX Sequence 416 AA;
 SQ
 Query Match 46.9%; Score 195; DB 8; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.5e-184;
 Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 222 QDHGALDCCVVVILSHGQASHLQFPGAVYGTGCPVSVKIVNIFNGTSCPSLGKPKL 281
 Db 222 QDHGALDCCVVVILSHGQASHLQFPGAVYGTGCPVSVKIVNIFNGTSCPSLGKPKL 281
 QY 282 FFIQACGGEQKHGFVASTSPEDSPGNSPEPDATPFQGLRTFDQLDAISSLTSPSDI 341
 Db 282 FFIQACGGEQKHGFVASTSPEDSPGNSPEPDATPFQGLRTFDQLDAISSLTSPSDI 341
 QY 342 FVSYSTPPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
 Db 342 FVSYSTPPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKOMP 401
 QY 402 GCNFKLKKLFFKTS 416
 Db 402 GCNFKLKKLFFKTS 416
 RESULT 13
 AAE00620
 ID AAE00620 standard; protein; 266 AA.
 AC AAE00620;
 XX
 XX 02-JUL-2001 (first entry)
 DT
 DE Human caspase-9.
 KW Human; caspase-9; interleukin-1 converting enzyme; ICE-IAP6; Mch6;
 KW cysteine protease; apoptosis; caspase expression cassette; metastasis;
 KW tumour; cathepsin B; urokinase; proliferation; gene therapy.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH

FT Cleavage-site 165..166 /label= Proteolytic_cleavage_site
FT Cleavage-site 180..181 /label= Proteolytic_cleavage_site
FT XX
PN WO200129232-A2.
XX
XX 26-APR-2001.
XX
XX 19-OCT-2000; 2000WO-US028941.
PF
XX 20-OCT-1999; 99US-0160559P.
PR
XX 14-AUG-2000; 2000US-0225564P.
XX
XX (SCIO-) SCTOS INC.
XX
XX
PI Cordell B, Li Y;
XX
DR WPI; 2001-290920/30.
DR N-PSDB; AAD03916.
XX

Novel fusion polypeptide comprising first and second caspase subunit separated by cleavage site not associated in nature with caspase subunit, useful for cloning gene encoding enzymes involved in proteolytic cleavage.
PT
PT
PT
PT
XX
PS Claim 4; Page 105-107; 116pp; English.
XX
XX The present amino acid sequence is human Caspase-9 also known as interleukin-1 converting enzyme (ICE) LAP6 and Mch6. Caspases are a family of cysteine proteases, that participate in the initiation and execution of apoptosis. Caspases exist as pro-enzymes, activated by cleavage into a large and small subunit, occurring after specific aspartic acid residues within the pro-enzyme sequence. The present invention relates to a method for functional cloning of genes encoding proteins or enzymes involved in proteolytic cleavage. The invention is based on the use of caspase expression cassettes comprising the coding sequence of a proteolytic cleavage site flanked by sequences encoding two caspase subunits. A fusion polypeptide comprising a first and a second caspase subunit, separated by a cleavage site not associated in nature, is useful for cloning gene encoding enzymes involved in proteolytic cleavage. An expression cassette containing fusion polypeptide is used to identify a mutant cell line deficient in an enzyme of interest and is also useful for diagnosis and suppression of proliferation or metastases of a tumour cell characterised by overexpression of a polypeptide (e.g. Cathepsin B or uronkinase, selectively expressed in the tumour cells). DNA encoding fusion polypeptide is used in gene therapy. Note: This sequence SEQ.ID.NO.18 is stated as being the same as that shown in Figure 18 (See AAE00606) in the specification. However these sequences differ at several positions
XX
SQ Sequence 266 AA;

Query Match 30.5%; Score 127; DB 4; Length 266;
Best Local Similarity 100.0%; Pred.No. 3.4e-117;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 EQKDHGEVASTSPEDSGSNPEPDATPFQGLRTFDQLDAISSLTPTSDIFVSVSTFP 349
Db |||||
140 EQKDHGEVASTSPEDSGSNPEPDATPFQGLRTFDQLDAISSLTPTSDIFVSVSTFP 199
QY 350 GFVSWRDPKSGWYVETLDDIFEQWAHSDQLSLLLRVANAVSVKGIYKQMPGCFNFLRK 409
Db |||||
200 GFVSWRDPKSGWYVETLDDIFEQWAHSDQLSLLLRVANAVSVKGIYKQMPGCFNFLRK 259
QY 410 KLFFKTS 416
Db |||||
260 KLFFKTS 266

RESULT 14
ADA10677
ID ADA10677 standard; protein; 401 AA.

XX
AC ADA10677;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human caspase-9 protein del316-330 mutant.
XX
XX Human; caspase-9; anti-HIV; nootropic; neuroprotective; vasotropic; cytostatic; immunosuppressive; inhibitor of apoptosis protein; IAP; caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3; Bir3 domain; apoptosis; AIDS; neurodegenerative disease; ischaemic injury; cancer; autoimmune disease; mutant; mutein.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 315..316
FT /note= "Residues 316-330 of the wild-type protein have been deleted"
FT
XX
XX US2002160975-A1.
PN
XX 31-OCT-2002.
PD
XX
XX 06-FEB-2002; 2002US-00068569.
PF
XX
XX 08-FEB-2001; 2001US-0267966P.
PR
XX 24-AUG-2001; 2001US-00939293.
PR
XX (UYJE-) UNIV JEFFERSON THOMAS.
PA
XX
XX Alnemri ES;
PI
XX
XX WPI; 2003-219992/21.
DR
XX
XX New nucleic acid molecules encoding a peptide or polypeptide that binds to a portion of an inhibitor of apoptosis protein, useful for inducing apoptosis and identifying inhibitors or enhancers of apoptosis for treating AIDS, or cancer.
PT
PT
XX
PS Claim 39; Page; 52pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule comprising a polynucleotide that encodes a polypeptide or peptide, or its variants that specifically binds to at least a portion of an inhibitor of apoptosis protein (IAP). Also included are a peptide or a polypeptide (comprising at least an N terminus sequence of caspase-9 N-terminal linker sequence, a first portion of a procaspase-9 that specifically binds at least a portion of an IAP and a second portion of a procaspase-9 containing a mutated active site, where the peptide or polypeptide specifically binds at least a portion of an IAP and lacks cysteine protease activity, and at least a portion of caspase-3, where the peptide or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by an IAP or an IAP Bir3 domain) or at least a portion of a mutated procaspase-9, which fails to undergo normal processing and possesses wild type caspase-9 enzymatic activity, a nucleic acid molecule comprising a polynucleotide sequence that encodes the caspase-9 N-terminal linker), an expression vector comprising any of the nucleic acids, a host cell containing the expression vector, an antibody that specifically binds to the peptide or polypeptide, an antibody that specifically binds to an epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis in a cell or stimulating apoptosis in a neoplastic or tumour cell, identifying an inhibitor or enhancer of caspase-mediated apoptosis, identifying a compound that inhibits the peptide or polypeptide, producing a compound for inhibiting or enhancing apoptosis in a cell, and a process for the manufacture of a compound for inhibiting or enhancing apoptosis in a cell. The nucleic acid molecules and peptides or polypeptides are useful for inducing apoptosis and identifying inhibitors or enhancers of apoptosis for treating AIDS, neurodegenerative diseases, ischaemic injury, cancer, autoimmune diseases. The present sequence represents the caspase-9 protein mutated to ablate the autocatalytic cleavage site in the linker region. Note: the present sequence is not

CC shown in the specification but was created by the indexer using the
 CC information in the claims and the wild type caspase-9 sequence.

XX SQ Sequence 401 AA;
 Query Match 29.8%; Score 124; DB 6; Length 401;
 Best Local Similarity 100.0%; Pred. No. 4.6e-114;
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 97 KLSKPTLENTLPVVLREPKPEVLPRTPVDIGSGGFDVGALSRLGNADLAYILS 156
 Db 97 KLSKPTLENTLPVVLREPKPEVLPRTPVDIGSGGFDVGALSRLGNADLAYILS 156
 QY 157 MEPGCHLIINNVNFCRESGLRTRTGSNIDCEKLRFRSSLHFVVEVKGDLTAKKMWLAL 216
 Db 157 MEPGCHLIINNVNFCRESGLRTRTGSNIDCEKLRFRSSLHFVVEVKGDLTAKKMWLAL 216
 QY 217 LELA 220
 Db 217 LELA 220

RESULT 15

ADA10675

XX ADA10675 standard; protein; 416 AA.

AC ADA10675;

XX 06-NOV-2003 (first entry)

XX Human caspase-9 protein D315A/D330A mutant.

XX Human; caspase-9; anti-HIV; neutrotropic; neuroprotective; vasotropic;
 KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease; mutant; mutetin.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 315 /note= "Wild-type Asp substituted by Ala"

FT Misc-difference 330 /note= "Wild-type Asp substituted by Ala"

XX US2002160975-A1.

XX 31-OCT-2002.

XX 06-FEB-2002; 2002US-00068569.

XX 08-FEB-2001; 2001US-0267966P.

XX 24-AUG-2001; 2001US-00939293.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;

XX WPI; 2003-219992/21.

XX New nucleic acid molecules encoding a peptide or polypeptide that binds
 PT to a portion of an inhibitor of apoptosis protein, useful for inducing
 PT apoptosis and identifying inhibitors or enhancers of apoptosis for
 PT treating AIDS, or cancer.

XX Claim 37; Page; 52pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising a
 CC polynucleotide that encodes a polypeptide or peptide, or its variants
 CC that specifically binds to at least a portion of an inhibitor of
 CC apoptosis protein (IAP). Also included are a peptide or a polypeptide

CC (comprising at least an N terminus sequence of caspase-9 N-terminal
 CC linker sequence, a first portion of a procaspase-9 that specifically
 CC binds at least a portion of an IAP and a second portion of a procaspase-9
 CC containing a mutated active site, where the peptide or polypeptide
 CC specifically binds at least a portion of an IAP and lacks cysteine
 CC protease activity, and at least a portion of caspase-3, where the peptide
 CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
 CC an IAP or an IAP Bir3 domain) or at least a portion of a mutated
 CC procaspase-9, which fails to undergo normal processing and possesses wild
 CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
 CC polynucleotide sequence that encodes the caspase-9 N-terminal linker), an
 CC expression vector comprising any of the nucleic acids, a host cell
 CC containing the expression vector, an antibody that specifically binds to
 CC the peptide or polypeptide, an antibody that specifically binds to an
 CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
 CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
 CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
 CC identifying a compound that inhibits the peptide or polypeptide,
 CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
 CC a process for the manufacture of a compound for inhibiting or enhancing
 CC apoptosis in a cell. The nucleic acid molecules and peptides or
 CC polypeptides are useful for inducing apoptosis and identifying inhibitors
 CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
 CC ischaemic injury, cancer, autoimmune diseases. The present sequence
 CC represents the caspase-9 protein mutated to ablate the autocatalytic
 CC cleavage site in the linker region. Note: the present sequence is not
 CC shown in the specification but was created by the indexer using the
 CC information in the claims and the wild type caspase-9 sequence.

XX SQ Sequence 416 AA;

Query Match 29.8%; Score 124; DB 6; Length 416;

Best Local Similarity 100.0%; Pred. No. 4.7e-114;

Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 KLSKPTLENTLPVVLREPKPEVLPRTPVDIGSGGFDVGALSRLGNADLAYILS 156

Db 97 KLSKPTLENTLPVVLREPKPEVLPRTPVDIGSGGFDVGALSRLGNADLAYILS 156

QY 157 MEPGCHLIINNVNFCRESGLRTRTGSNIDCEKLRFRSSLHFVVEVKGDLTAKKMWLAL 216

Db 157 MEPGCHLIINNVNFCRESGLRTRTGSNIDCEKLRFRSSLHFVVEVKGDLTAKKMWLAL 216

QY 217 LELA 220

Db 217 LELA 220

RESULT 16

ADA10676

XX ADA10676 standard; protein; 416 AA.

AC ADA10676;

XX 06-NOV-2003 (first entry)

XX Human caspase-9 protein E306A/D315A/D330A mutant.

XX Human; caspase-9; anti-HIV; neutrotropic; neuroprotective; vasotropic;
 KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease; mutant; mutetin.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 306 /note= "Wild-type Glu substituted by Ala"

FT Misc-difference 315 /note= "Wild-type Asp substituted by Ala"

FT Misc-difference 330

CC polypeptides are useful for inducing apoptosis and identifying inhibitors
CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
CC ischaemic injury, cancer, autoimmune diseases. The present sequence
CC represents the caspase-9 protein mutated to ablate the autocatalytic
CC cleavage site in the linker region. Note: the present sequence is not
CC shown in the specification but was created by the indexer using the
CC information in the claims and the wild type caspase-9 sequence.

XX SQ Sequence 416 AA;

Query Match 29.8%; Score 124; DB 6; Length 416;
Best Local Similarity 100.0%; Pred. No. 4.7e-114;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 KLSKPTLENTPTVVLRLPEIRKPEVLRPETPRPDVIGSGGFDVCALESIRGNADLAYILS 156

DB 97 KLSKPTLENTPTVVLRLPEIRKPEVLRPETPRPDVIGSGGFDVCALESIRGNADLAYILS 156

QY 157 MEPGCHCLINNVNFCRESGLRTGTGNSIDCEKLRFRFSSLHFWVEVKGDLTAKKMVLAL 216

DB 157 MEPGCHCLINNVNFCRESGLRTGTGNSIDCEKLRFRFSSLHFWVEVKGDLTAKKMVLAL 216

QY 217 LEIA 220

DB 217 LEIA 220

RESULT 18

ABJ04760
ID ABJ04760 standard; protein; 93 AA.

XX AC ABJ04760;

XX AC ABJ04760;

DT 16-OCT-2002 (first entry)

DE Caspase-9 protein sequence SEQ ID No 27.

XX Intracellular signaling polypeptide; Nod2; Crohn's disease; mutation;
KW cytosine residue insertion; nuclear factor; NF-B activation; NF-kappa B;
KW RICK signaling; gene therapy; transgenic plant; plant.
XX Homo sapiens.

XX W0200244426-A2.

XX 06-JUN-2002.

XX 26-OCT-2001; 2001WO-US051068.

XX 30-OCT-2000; 2000US-0244266P.

XX 25-APR-2001; 2001US-0286316P.

XX 26-OCT-2001; 2001US-00286316.

XX (UNMI) UNIV MICHIGAN.

XX (UYCH-) UNIV CHICAGO.

XX Nunez G, Inohara N, Ogura Y, Cho J, Nicolae DL, Bonen D;

XX WPI; 2002-547704/58.

XX New isolated intracellular signaling polypeptide, termed Nod2, useful for
XX producing an antibody that recognizes Nod2, and as a target for screening
XX drugs.

XX Disclosure; Fig 2; 316pp; English.

XX The invention relates to an isolated intracellular signaling polypeptide,
XX termed Nod2, comprising a sequence of 1007 or 1040 amino acids, given in
XX the specification. The nucleic acid encoding the isolated protein is
XX useful for identifying subjects at risk of developing Crohn's disease by
XX providing a nucleic acid from the subject, where the nucleic acid
XX comprises a Nod2 gene, and detecting the presence or absence of one or
XX more variations in the Nod2 gene. Detecting comprises comparing the

CC sequence of the nucleic acid to the sequence of a wild-type Nod2 nucleic
CC acid. Detection is accomplished by hybridisation analysis. The method
CC further comprises determining if the subject is at risk of developing
CC Crohn's disease based on the presence or absence of the variations, and
CC determining a genotype relative risk or a population attributable risk
CC for the subject. The variation is a polymorphism or a mutation,
CC preferably a cytosine residue insertion, where the mutation causes a
CC deletion of a Leu-Arg-Arg repeat of Nod2. The variation results in
CC increased nuclear factor (NF)-B activation. The variation is selected
CC from the sequences of the Nod2 gene. The isolated protein is useful as a
CC target for screening drugs that can alter, for example, RICK signaling,
CC and thus the physiological effects of NF-kappa B. The Nod2 gene is useful
CC for producing the isolated protein by recombinant techniques, as starting
CC nucleic acids for directed evolution, for gene therapy, or to decrease
CC the level of Nod2 protein or mRNA in transgenic plants, plant tissues, or
CC plant cells as compared to wild-type plants, plant tissues or plant
CC cells. This sequence represents a Nod2 related protein of the invention
XX

XX SQ Sequence 93 AA;

Query Match 22.4%; Score 93; DB 5; Length 93;

Best Local Similarity 100.0%; Pred. No. 7.6e-84;

Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRRLLRRCLRLVLEELQVDLQDLVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

DB 1 MDEADRRLLRRCLRLVLEELQVDLQDLVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNR 93

DB 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNR 93

RESULT 19

ABP71130

ID ABP71130 standard; protein; 42 AA.

XX AC ABP71130;

XX AC ABP71130;

DT 14-APR-2003 (first entry)

XX Mch6 CARD protein fragment.

XX BTF3; cell death; apoptosis; basic transcription factor; cytostatic;

XX neotropic; neuroprotective; antiparkinsonian; antiarteriosclerotic;

XX antirheumatic; antiarthritic; gene therapy; CARD; Mch6.

XX Unidentified.

XX W0200295001-A2.

XX 28-NOV-2002.

XX 21-MAY-2002; 2002WO-US016230.

XX 21-MAY-2001; 2001US-0292559P.

XX (REGC) UNIV CALIFORNIA.

XX Rothman JH, Bloss T, Witz E;

XX WPI; 2003-167228/16.

XX Inhibiting or increasing programmed cell death of a cell, for treating

XX e.g. cancer, comprises upregulating or inhibiting, respectively, the

XX expression or activity of basic transcription factor (BTF)3 or its

XX homolog in the cell.

XX Example; Fig 2B; 84pp; English.

XX The invention relates to inhibiting or increasing programmed cell death
XX of a cell. The method involves upregulating or inhibiting, respectively,
XX the expression or activity of basic transcription factor (BTF)3 or its

CC homologue in the cell. The BTF3 polypeptides and nucleic acids are useful
 CC for inhibiting or increasing programmed cell death. They are used for
 CC screening for an agent that increases or inhibits programmed cell death
 CC or pre-screening for an agent that modulates programmed cell death. The
 CC screened agent that increases or inhibits programmed cell death, is used
 CC for diagnosing or treating cancer or neurodegenerative diseases (e.g.
 CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease
 CC or multiple sclerosis), atherosclerosis, or rheumatoid arthritis.
 CC Sequences ABP1124-135 represent peptide fragments various CARD proteins
 XX
 XX Sequence 42 AA;

Query Match 10.1%; Score 42; DB 6; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.6e-33;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 GSGSRDQARQLIIDLTRGSQLPLFISCLDGTQDMLASF 88

Db 1 GSGSRDQARQLIIDLTRGSQLPLFISCLDGTQDMLASF 42

RESULT 20
 ADA10663
 ID ADA10663 standard; peptide; 32 AA.

AC ADA10663;

XX 06-NOV-2003 (first entry)

XX Human procaspase -9 amino acids 303-324.

XX caspase-9; anti-HIV; notropic; neuroprotective; vasotropic; cytostatic;
 KW immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease; human.

XX Homo sapiens.

OS US2002160975-A1.

XX 31-OCT-2002.

XX 06-FEB-2002; 2002US-00068569.

XX 08-FEB-2001; 2001US-0267966P.

XX 24-AUG-2001; 2001US-00939293.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;

XX WPI; 2003-219992/21.

XX New nucleic acid molecules encoding a peptide or polypeptide that binds
 PT to a portion of an inhibitor of apoptosis protein, useful for inducing
 PT apoptosis and identifying inhibitors or enhancers of apoptosis for
 PT treating AIDS, or cancer.

XX Example 1; Fig 1; 52pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising a
 CC polynucleotide that encodes a polypeptide or peptide, or its variants
 CC that specifically binds to at least a portion of an inhibitor of
 CC apoptosis protein (IAP). Also included are a peptide or a polypeptide
 CC (comprising at least an N terminus sequence of caspase-9 N-terminal
 CC linker sequence, a first portion of a procaspase-9 that specifically
 CC binds at least a portion of an IAP and a second portion of a procaspase-9
 CC containing a mutated active site, where the peptide or polypeptide
 CC specifically binds at least a portion of an IAP and lacks cysteine
 CC protease activity, and at least a portion of caspase-3, where the peptide
 CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
 CC an IAP or an IAP Bir3 domain) or at least a portion of a mutated

CC procaspase-9, which fails to undergo normal processing and possesses wild
 CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
 CC polynucleotide sequence that encodes the caspase-9 N-terminal linker, an
 CC expression vector comprising any of the nucleic acids, a host cell
 CC containing the expression vector, an antibody that specifically binds to
 CC the peptide or polypeptide, an antibody that specifically binds to an
 CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
 CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
 CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
 CC identifying a compound that inhibits the peptide or polypeptide,
 CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
 CC a process for the manufacture of a compound for inhibiting or enhancing
 CC apoptosis in a cell. The nucleic acid molecules and peptides or
 CC polypeptides are useful for inducing apoptosis and identifying inhibitors
 CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
 CC ischaemic injury, cancer, autoimmune diseases. The present sequence
 CC represents amino acids 303-324 of human procaspase-9 containing the
 CC linker region and autocatalytic sites.

XX Sequence 32 AA;

Query Match 7.7%; Score 32; DB 6; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.1e-23;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 PEDESGSNPEPDATPFQEGLTFTDQLDAISS 334

Db 1 PEDESGSNPEPDATPFQEGLTFTDQLDAISS 32

RESULT 21

ADA10667

ID ADA10667 standard; peptide; 32 AA.

XX ADA10667;

XX 06-NOV-2003 (first entry)

XX Human procaspase -9 linker peptide.

XX caspase-9; anti-HIV; notropic; neuroprotective; vasotropic; cytostatic;
 KW immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease; human.

XX Homo sapiens.

OS US2002160975-A1.

XX 31-OCT-2002.

XX 06-FEB-2002; 2002US-00068569.

XX 08-FEB-2001; 2001US-0267966P.

XX 24-AUG-2001; 2001US-00939293.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;

XX WPI; 2003-219992/21.

XX New nucleic acid molecules encoding a peptide or polypeptide that binds
 PT to a portion of an inhibitor of apoptosis protein, useful for inducing
 PT apoptosis and identifying inhibitors or enhancers of apoptosis for
 PT treating AIDS, or cancer.

XX Example 3; Page 22; 52pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising a
 CC polynucleotide that encodes a polypeptide or peptide, or its variants
 CC that specifically binds to at least a portion of an inhibitor of

CC apoptosis protein (IAP). Also included are a peptide or a polypeptide
 CC (comprising at least an N terminus sequence of caspase-9 N-terminal
 CC linker sequence, a first portion of a procaspase-9 that specifically
 CC binds at least a portion of an IAP and a second portion of a procaspase-9
 CC containing a mutated active site, where the peptide or polypeptide
 CC specifically binds at least a portion of an IAP and lacks cysteine
 CC protease activity, and at least a portion of caspase-3, where the peptide
 CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
 CC an IAP or an IAP Bir3 domain) or at least a portion of a mutated
 CC procaspase-9, which fails to undergo normal processing and possesses wild
 CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
 CC polynucleotide sequence that encodes the caspase-9 N-terminal linker, an
 CC expression vector comprising any of the nucleic acids, a host cell
 CC containing the expression vector, an antibody that specifically binds to
 CC the peptide or polypeptide, an antibody that specifically binds to an
 CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
 CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
 CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
 CC identifying a compound that inhibits the peptide or polypeptide,
 CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
 CC a process for the manufacture of a compound for inhibiting or enhancing
 CC apoptosis in a cell. The nucleic acid molecules and peptides or
 CC polypeptides are useful for inducing apoptosis and identifying inhibitors
 CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
 CC ischaemic injury, cancer, autoimmune diseases. The present sequence
 CC represents human procaspase-9 linker region.

XX SQ Sequence 32 AA;

Query Match 7.7%; Score 32; DB 6; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.1e-23;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 PEDESGNPEPDATPQEGLTDPQLDAISS 334
 |||||
 DB 1 PEDESGNPEPDATPQEGLTDPQLDAISS 32

RESULT 22

ABP71113
 ID ABP71113 standard; peptide; 19 AA.

XX AC ABP71113;

XX DT 14-APR-2003 (first entry)

XX DE Mch6 protein CARD region fragment.

XX KW BTF3; cell death; apoptosis; basic transcription factor; cytostatic;
 XX KW neurotropic; neuroprotective; antiparkinsonian; antiarteriosclerotic;
 XX KW antirheumatic; antiarthritic; gene therapy; CARD; Mch6.

XX OS Unidentified.

XX PN WO200295001-A2.

XX XX 28-NOV-2002.

XX PF 21-MAY-2002; 2002WO-US016230.

XX PR 21-MAY-2001; 2001US-0232559P.

XX PA (REGC) UNIV CALIFORNIA.

XX FI Rothman JH, Bloss T, Witze E;

XX XX WPI; 2003-167228/16.

XX PT Inhibiting or increasing programmed cell death of a cell, for treating
 PT e.g. cancer, comprises upregulating or inhibiting, respectively, the
 PT expression or activity of basic transcription factor (BTF)3 or its
 PT homolog in the cell.

PS Example; Fig 2A; 84pp; English.

XX CC The invention relates to inhibiting or increasing programmed cell death
 CC of a cell. The method involves upregulating or inhibiting, respectively,
 CC the expression or activity of basic transcription factor (BTF)3 or its
 CC homologue in the cell. The BTF3 polypeptides and nucleic acids are useful
 CC for inhibiting or increasing programmed cell death. They are used for
 CC screening for an agent that increases or inhibits programmed cell death
 CC or pre-screening for an agent that modulates programmed cell death. The
 CC screened agent that increases or inhibits programmed cell death, is used
 CC for diagnosing or treating cancer or neurodegenerative diseases (e.g.
 CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease
 CC or multiple sclerosis), atherosclerosis, or rheumatoid arthritis.

CC Sequences ABP71106-123 represent CARD regions of various CARD proteins

XX SQ Sequence 19 AA;

Query Match 4.6%; Score 19; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.6e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 WDVLLSRELFRPHMIEDIQ 44
 |||||
 DB 1 WDVLLSRELFRPHMIEDIQ 19

RESULT 23

AAAY21739

ID AAY21739 standard; peptide; 15 AA.

XX AC AAY21739;

XX DT 10-SEP-1999 (first entry)

XX DE Conserved peptide sequence of Mch6 (caspase-9).

XX KW Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
 XX KW autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
 XX KW tumour cell; myocardial infarction; human.

XX OS Homo sapiens.

XX PN WO9935277-A2.

XX XX 15-JUL-1999.

XX PF 11-JAN-1999; 99WO-US000632.

XX PR 09-JAN-1998; 98US-0070987P.

XX XX (UWJE-) UNIV JEFFERSON THOMAS.

XX FI Alnemri ES;

XX DR WPI; 1999-419353/35.

XX PT New isolated nucleic acid molecule encoding a rev-caspase - used for
 PT screening and identifying inhibitors or enhancers for treating cancer or
 PT autoimmune disease.

XX PS Disclosure; Fig 6; 74pp; English.

XX CC The invention relates to nucleic acid molecules encoding rev-caspases.
 CC Rev-caspases are cysteine proteases that specifically cleave proteins
 CC after Asp residues and is expressed as a zymogen, in which the small
 CC subunit is N-terminal to a large subunit. A gene delivery vehicle
 CC comprising a rev-caspase coding sequence is useful for the treatment of
 CC cancer, where the gene delivery vehicle is internalised by tumour cells.
 CC The gene delivery vehicle can also be used to treat autoimmune diseases.
 CC Cells transfected with a rev-caspase expressing vector can be used in
 CC identification of inhibitors or enhancers of caspase-mediated apoptosis.
 CC In vitro translated rev-caspase can be used to identify an inhibitor or
 CC enhancer of caspase processing activity. Caspase inhibitors are useful

OS Homo sapiens.
 XX WO2003006680-A2.
 PN XX
 XX 23-JAN-2003.
 PD XX
 XX 15-JUL-2002; 2002WO-US022658.
 XX
 XX 13-JUL-2001; 2001US-0305378P.
 PR 14-DEC-2001; 2001US-0340163P.
 XX
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 PA Alnemri ES;
 PI WPI; 2003-221760/21.
 XX
 XX New Omi nucleic acids and peptides that bind to an inhibitor of apoptosis
 PT proteins, useful for regulating or altering caspase-mediated apoptosis
 PT and for treating cancer, tumor, or autoimmune diseases.
 XX
 XX Example 2; Fig 6; 83pp; English.
 PS
 XX The invention relates to polynucleotides encoding an Omi (serine
 CC protease) peptide or polypeptide. The Omi peptide specifically binds to a
 CC portion of an inhibitor of Apoptosis Protein (IAP). The Omi polypeptide
 CC induces caspase-independent apoptosis, or fails to have serine protease
 CC activity. The Omi peptides are useful for regulating or altering
 CC apoptosis, specifically caspase-mediated apoptosis, and as immunogens for
 CC raising antibodies. Enhancers of apoptosis are useful for treating
 CC cancers, tumors or for destroying cells that mediate autoimmune
 CC diseases. Compositions may also be used for the treatment of diseases
 CC associated with inappropriate activation of apoptosis such as
 CC neurodegenerative diseases and ischaemic injury. The antibodies can be
 CC used in isolating Omi peptides, polypeptides and their variants, in
 CC identifying molecules that interact with Omi peptides and polypeptides,
 CC and in inhibiting or enhancing the biological activity of Omi peptides
 CC and polypeptides. Sequences ABP71310-315 represent fragments of various
 CC IAP-binding proteins, used to determine Omi as a IAP-binding protein
 XX
 SQ Sequence 15 AA;
 Query Match 3.6%; Score 15; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.2e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 316 ATPFQEGRLTFDQLD 330
 Db |||||
 1 ATPFQEGRLTFDQLD 15
 RESULT 27
 ADA10656
 ID ADA10656 standard; peptide; 15 AA.
 XX
 AC ADA10656;
 XX
 XX 06-NOV-2003 (first entry)
 DT
 XX Mouse caspase-9-p12 subunit N-terminus #1.
 DE
 XX caspase-9; anti-HIV; neurotropic; neuroprotective; vasotrophic; cytostatic;
 XX immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease; mouse; p12 subunit.
 XX
 OS Mus musculus.
 XX
 XX US2002160975-A1.
 PN
 XX 31-OCT-2002.
 PD
 XX

PF 06-FEB-2002; 2002US-00068569.
 XX
 PR 08-FEB-2001; 2001US-0267966P.
 PR 24-AUG-2001; 2001US-00933293.
 XX
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 PA Alnemri ES;
 XX WPI; 2003-219992/21.
 XX
 XX New nucleic acid molecules encoding a peptide or polypeptide that binds
 PT to a portion of an inhibitor of apoptosis protein, useful for inducing
 PT apoptosis and identifying inhibitors or enhancers of apoptosis for
 PT treating AIDS, or cancer.
 XX
 PS Claim 27; Fig 9; 52pp; English.
 XX
 XX The invention relates to an isolated nucleic acid molecule comprising a
 CC polynucleotide that encodes a polypeptide or peptide, or its variants
 CC that specifically binds to at least a portion of an inhibitor of
 CC apoptosis protein (IAP). Also included are a peptide or a polypeptide
 CC comprising at least an N terminus sequence of caspase-9 N-terminal
 CC linker sequence, a first portion of a procaspase-9 that specifically
 CC binds at least a portion of an IAP and a second portion of a procaspase-9
 CC containing a mutated active site, where the peptide or polypeptide
 CC specifically binds at least a portion of an IAP and lacks cysteine
 CC protease activity, and at least a portion of caspase-3, where the peptide
 CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
 CC an IAP or an IAP Bir3 domain) or at least a portion of a mutated
 CC type caspase-9, which fails to undergo normal processing and possesses wild
 CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
 CC polynucleotide sequence that encodes the caspase-9 N-terminal linker), an
 CC expression vector comprising any of the nucleic acids, a host cell
 CC containing the expression vector, an antibody that specifically binds to
 CC the peptide or polypeptide, an antibody that specifically binds to an
 CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
 CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
 CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
 CC identifying a compound that inhibits the peptide or polypeptide,
 CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
 CC a process for the manufacture of a compound for inhibiting or enhancing
 CC apoptosis in a cell. The nucleic acid molecules and peptides or
 CC polypeptides are useful for inducing apoptosis and identifying inhibitors
 CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
 CC ischaemic injury, cancer, autoimmune diseases. The present sequence
 CC represents the N-terminus of an IAP protein containing a Bir3 domain.
 XX
 SQ Sequence 15 AA;
 Query Match 3.6%; Score 15; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.2e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 316 ATPFQEGRLTFDQLD 330
 Db |||||
 1 ATPFQEGRLTFDQLD 15
 RESULT 28
 ADA10651
 ID ADA10651 standard; peptide; 15 AA.
 XX
 AC ADA10651;
 XX
 XX 06-NOV-2003 (first entry)
 DT
 XX Human caspase-9-p12 subunit N-terminus #1.
 DE
 XX caspase-9; anti-HIV; neurotropic; neuroprotective; vasotrophic; cytostatic;
 KW immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW

KW ischaemic injury; cancer; autoimmune disease; Human; p12 subunit.

OS Homo sapiens.

XX US2002160975-A1.

PN 31-OCT-2002.

XX 06-FEB-2002; 2002US-00068569.

XX 08-FEB-2001; 2001US-0267966P.

PR 24-AUG-2001; 2001US-00939293.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;

XX WPI; 2003-219992/21.

XX New nucleic acid molecules encoding a peptide or polypeptide that binds to a portion of an inhibitor of apoptosis protein, useful for inducing apoptosis and identifying inhibitors or enhancers of apoptosis for treating AIDS, or cancer.

PS Claim 27; Fig 9; 52pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising a polynucleotide that encodes a polypeptide or peptide, or its variants that specifically binds to at least a portion of an inhibitor of apoptosis protein (IAP). Also included are a peptide or a polypeptide (comprising at least an N terminus sequence of caspase-9 N-terminal linker sequence, a first portion of a procaspase-9 that specifically binds to at least a portion of an IAP and a second portion of a procaspase-9 containing a mutated active site, where the peptide or polypeptide specifically binds to at least a portion of an IAP and lacks cysteine protease activity, and at least a portion of caspase-3 where the peptide or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by an IAP or an IAP Bir3 domain) or at least a portion of a mutated procaspase-9, which fails to undergo normal processing and possesses wild type caspase-9 enzymatic activity, a nucleic acid molecule comprising a polynucleotide sequence that encodes the caspase-9 N-terminal linker, an expression vector comprising any of the nucleic acids, a host cell containing the expression vector, an antibody that specifically binds to the peptide or polypeptide, an antibody that specifically binds to an epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis in a cell or stimulating apoptosis in a neoplastic or tumour cell, identifying an inhibitor or enhancer of caspase-mediated apoptosis, identifying a compound that inhibits the peptide or polypeptide, producing a compound for inhibiting or enhancing apoptosis in a cell, and a process for the manufacture of a compound for inhibiting or enhancing apoptosis in a cell. The nucleic acid molecules and peptides or polypeptides are useful for inducing apoptosis and identifying inhibitors or enhancers of apoptosis for treating AIDS, neurodegenerative diseases, ischaemic injury, cancer, autoimmune diseases. The present sequence represents the N-terminus of an IAP protein containing a Bir3 domain.

XX Sequence 15 AA;

Query Match 3.6%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 ATPFOEGLRTFDQLD 330

DB 1 ATPFOEGLRTFDQLD 15

RESULT 29

AAE08939

ID AAE08939 standard; peptide; 46 AA.

XX AAE08939;

AC AAE08939;

XX

DT 15-NOV-2001 (first entry)

XX Mammalian ced-3 homologue 6 (Mch6) peptide.

XX Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer; aspartate-specific cysteine protease; ASCP; apoptosis; therapy; autoimmune disease; cerebellar degeneration; Alzheimer's disease; cytostatic; Parkinson's disease; immunomodulator; antimicrobial; viral infection; cell death-mediated disease; neuroprotective.

XX Unidentified.

XX US6271361-B1.

XX 07-AUG-2001.

XX 25-FEB-1999; 99US-00257218.

XX 29-MAY-1997; 97US-00865579.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES, Fernandes-Alnemri T, Litwack G;

XX WPI; 2001-528686/58.

XX New apoptotic genes and their apoptotic protease products, useful for modulating apoptosis for the therapeutic treatment of human diseases, e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's disease.

XX Example 1; Fig 2; 36pp; English.

XX The invention relates to an isolated gene encoding apoptotic protease, mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the aspartate-specific cysteine protease (ASCP) family. Mch6 DNA and protein sequences are useful for modulating apoptosis for the therapeutic treatment of human diseases. Mch6 sequences are useful for upregulating apoptosis (e.g. for treating cancers, autoimmune disease or viral infections) or downregulating apoptosis (e.g. for treating Alzheimer's disease, Parkinson's disease or cerebellar degeneration). The Mch6 sequence is useful for diagnosing, treating or reducing the severity of cell death-mediated diseases, as well as other diseases mediated by either increased or decreased programmed cell death. The present amino acid sequence is Mch6 peptide

XX Sequence 46 AA;

Query Match 3.6%; Score 15; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 GFVSWRDPKSGSWYV 364

DB 32 GFVSWRDPKSGSWYV 46

RESULT 30

ADE52024

ID ADE52024 standard; protein; 46 AA.

XX ADE52024;

XX 29-JAN-2004 (first entry)

XX Aspartate-specific cysteine protease Mch6 fragment.

XX cytosolic; virucide; nontropic; neuroprotective; antiparkinsonian; cardiant; apoptosis modulator; aspartate-specific cysteine protease; gene therapy; aspartate-specific cysteine protease agonist; aspartate-specific cysteine protease antagonist; Mch6; mammalian ced-3 homologue 6; apoptosis; cancer; viral infection; degenerative disorder; Alzheimers disease; Parkinsons disease;

KW myocardial infarction; human; ASPC.
 XX Homo sapiens.
 OS
 PN US2002183504-A1.
 XX
 XX
 PD 05-DEC-2002.
 XX
 XX 29-JAN-2002; 2002US-00059749.
 XX
 XX 29-MAY-1997; 97US-00865579.
 PR
 PR 25-FEB-1999; 99US-00257218.
 PR
 PR 22-DEC-2000; 2000US-00746731.
 XX
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 PA
 XX
 XX Alnemri ES, Fernandes-Alnemri T, Litwack G;
 PI
 PI WPI; 2004-040943/04.
 DR
 XX New isolated gene encoding a mammalian ced-3 homolog 6, for modulating
 PT apoptosis for the therapeutic treatment of human diseases, such as
 PT cancers and degenerative disorders.
 PT
 XX
 XX Example 1; SEQ ID NO 6; 15pp; English.
 PS
 XX The invention describes an isolated gene (I) encoding Mch6 (mammalian ced
 CC -3 homologue 6), or a functional fragment of it. (I) And the polypeptide
 CC encoded by (I) is used to modulate apoptosis for the therapeutic
 CC treatment of human diseases. (I) Is used to prepared a recombinant
 CC aspartate-specific cysteine protease, that it encodes. The recombinant
 CC protease can be used to screen for Mch6 inhibitors. Disorders involving
 CC apoptosis that can be diagnosed or treated by (I) or the polypeptide it
 CC encodes, including cancers, viral infections, degenerative disorders,
 CC such as Alzheimers and Parkinsons disease, and myocardial infarction.
 CC This is the amino acid sequence of a human aspartate-specific cysteine
 CC protease (ASCP) fragment used in a comparison with other ASCP family
 CC members.
 CC
 XX
 XX Sequence 46 AA;
 SQ
 Query Match 3.6%; Score 15; DB 8; Length 46;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 350 GFVSWRDPKSGSWTV 364
 |||||
 Db 32 GFVSWRDPKSGSWTV 46
 |||||
 RESULT 31
 AAM97045
 ID AAM97045 standard; peptide; 14 AA.
 XX
 AC AAM97045;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human peptide #320 encoded by a SNP oligonucleotide.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200147944-A2.
 PN
 XX

PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-US035498.
 XX
 XX 28-DEC-1999; 99US-0173419P.
 PR
 PR 27-DEC-2000; 2000US-00173419.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX Shimkets RA, Leach M;
 PI
 PI WPI; 2001-465210/50.
 DR
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PR oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
 PT autoimmune diseases and infections.
 PT
 XX
 XX Disclosure; Page 3738; 4143pp; English.
 PS
 XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis-related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotide and the peptide encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 3.4%; Score 14; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 35 FRPHMIEDIQRAGS 49
 |||||
 Db 1 FRPHMIEDIQRAGS 14
 |||||
 RESULT 32
 AAU08321
 ID AAU08321 standard; peptide; 15 AA.
 XX
 AC AAU08321;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 DE Human MCH6 conserved sequence #6.
 XX
 KW Human; aspartate-specific cysteine protease; MCH6; nootropic;
 KW neuroprotective; anti-Parkinsonian; antianemic; vasotropic; cardiant;
 KW cerebrotective; mammalian ced-3 homologue 6; gene therapy; apoptosis;
 KW Alzheimer's disease; Parkinson's disease; retinitis pigmentosa;
 KW cerebellar degeneration; myelodysplastic syndrome; aplastic anaemia;
 KW ischaemic injury; myocardial infarction; stroke; reperfusion injury;
 KW amyotrophic lateral sclerosis; conserved sequence.
 XX
 OS Homo sapiens.
 XX
 XX US2001016345-A1.
 PN
 XX 23-AUG-2001.
 PD
 XX 22-DEC-2000; 2000US-00746731.
 PF
 XX

PR 29-MAY-1997; 97US-00865579.
 PR 25-FEB-1999; 99US-00257218.
 PA (ALNE//) ALNEMRI E S.
 PA (FERN//) FERNANDES-ALNEMRI T.
 PA (LITW//) LITWACK G.
 XX
 PI Alnemri ES, Fernandes-Alnemri T, Litwack G;
 XX
 DR WPI; 2001-535542/59.
 XX
 XX New Mch6 polypeptides and genes encoding the polypeptides useful for
 PT diagnosing, treating or reducing the severity of cell death-mediated
 PT diseases such as neurodegenerative diseases e.g. Alzheimer's disease,
 PT Parkinson's disease.
 XX
 XX Example 1; Fig 2; 15pp; English.
 PS
 XX The invention relates to an isolated gene encoding MCH6 (mammalian ced-3
 CC homologue 6) an aspartate-specific cysteine protease and the MCH6
 CC polypeptide. The MCH6-encoding nucleic acids and polypeptides can be used
 CC to diagnose, treat (e.g. by gene therapy) or reduce the severity of cell
 CC death-mediated diseases (i.e. apoptotic) such as neurodegenerative
 CC diseases e.g. Alzheimer's disease, Parkinson's disease, amyotrophic
 CC lateral sclerosis, retinitis pigmentosa and cerebellar degeneration, and
 CC myelodysplastic syndromes, e.g. aplastic anaemia, ischaemic injury,
 CC myocardial infarction, stroke and reperfusion injury. The MCH6-encoding
 CC nucleic acids and polypeptides can also be used to diagnose or generate
 CC reagents to diagnose diseases mediated or characterised by programmed
 CC cell death. A purified recombinant MCH6 protein can be used to measure
 CC hydrolysis rates for various substrates such as DEVD-AMC and YVAD-AMC in
 CC a continuous fluorometric assay. The present sequence represents a
 CC conserved sequence from human MCH6 indicating that MCH6 is a member of
 CC the Ced-like subfamily of proteases
 XX
 SQ Sequence 15 AA;
 Query Match 2.9%; Score 12; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0004;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 350 GFVSWRDPKSGS 361
 Db |||||
 1 GFVSWRDPKSGS 12
 RESULT 33
 AA89198
 ID AA89198 standard; protein; 299 AA.
 XX
 AC AA89198;
 XX
 DT 17-MAR-1999 (first entry)
 XX
 DE Aspartate-specific cysteine protease, Caspase-1.
 XX
 KW Caspase-1; Spodoptera frugiperda; Sf; insect; nuclear immunophilin;
 KW CED-3 subfamily; aspartate-specific cysteine protease; ASCP; apoptosis.
 XX
 OS Spodoptera frugiperda.
 XX
 XX Key Location/Qualifiers
 FH Cleavage-site 28..29
 FT Cleavage-site 184..185
 FT Cleavage-site 195..196
 XX
 PN US5858778-A.
 XX
 XX 12-JAN-1999.
 PD
 XX 27-DEC-1996; 96US-00773608.
 PF
 XX 27-DEC-1996; 96US-00773608.
 PR

XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Litwack G, Alnemri ES, Fernandes-Alnemri T;
 XX
 DR WPI; 1999-119894/10.
 DR N-PSDB; AAV80061.
 XX
 PT Isolated aspartate-specific cysteine protease; Caspase-1 - obtained from
 PT Spodoptera frugiperda, used to develop screening assays for compounds
 PT which can inhibit or enhance apoptosis.
 XX
 XX Claim 1; Fig 1A; 22pp; English.
 PS
 XX This represents a Caspase-1 pro-enzyme, a novel Spodoptera frugiperda
 CC (Sf) insect cell nuclear immunophilin which belongs to the CED-3
 CC subfamily of aspartate-specific cysteine proteases (ASCPs). A host cell
 CC containing an expression vector comprising the Caspase-1 nucleic acid can
 CC be used for the recombinant production of the protein. The products can
 CC be used for screening for compounds which can inhibit or enhance Caspase-
 CC 1 activity and which can be used to inhibit or enhance, respectively,
 CC apoptosis. The Caspase-1 can also be used to identify proteins which are
 CC processed by it. The products can also be used for the production of
 CC antibodies and for the production of transgenic animals
 XX
 SQ Sequence 299 AA;
 Query Match 2.6%; Score 11; DB 2; Length 299;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 277 GRPKLFFFIQAC 287
 Db |||||
 168 GRPKLFFFIQAC 178
 RESULT 34
 ABB61468
 ID ABB61468 standard; protein; 323 AA.
 XX
 AC ABB61468;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 11196.
 XX
 KW Drosophila; developmental biology; cell signaling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI
 XX WPI; 2001-658860/75.
 DR
 DR N-PSDB; ABL05571.
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 11196; 21pp + Sequence Listing; English.
 XX

CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 323 AA;

Query Match 2.6%; Score 11; DB 4; Length 323;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFIOAC 287
|||||
Db 186 GKPKLFFIOAC 196

RESULT 35
ABB58379
ID ABB58379 standard; protein; 339 AA.
XX
AC ABB58379;
XX
XX 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 1929.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX
OS Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX N-PSDB; ABL02482.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX
XX Disclosure; SEQ ID NO 1929; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 339 AA;

Query Match 2.6%; Score 11; DB 4; Length 339;

Best Local Similarity 100.0%; Pred. No. 0.062; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;

QY 277 GKPKLFFIOAC 287
|||||
Db 201 GKPKLFFIOAC 211

RESULT 36
ABP71122
ID ABP71122 standard; peptide; 10 AA.

XX
XX AC ABP71122;
XX
XX 14-APR-2003 (first entry)
XX
XX Mch6 protein CARD region fragment.
XX
XX BTF3; cell death; apoptosis; basic transcription factor; cytostatic;
XX nontropic; neuroprotective; antiparkinsonian; antiarteriosclerotic;
XX antirheumatic; antiarthritic; gene therapy; CARD; Mch6.

XX Unidentified.

XX WO200295001-A2.
XX
XX 28-NOV-2002.
XX
XX 21-MAY-2002; 2002WO-US016230.
XX
XX 21-MAY-2001; 2001US-0292559P.

XX (REGC) UNIV CALIFORNIA.
XX
XX Rothman JH, Bloss T, Witze E;
XX
XX WPI; 2003-167228/16.
XX

PT Inhibiting or increasing programmed cell death of a cell, for treating
PT e.g. cancer, comprises upregulating or inhibiting, respectively, the
PT expression or activity of basic transcription factor (BTF)3 or its
PT homolog in the cell.
XX
XX Example; Fig 2A; 84pp; English.

PS The invention relates to inhibiting or increasing programmed cell death
CC of a cell. The method involves upregulating or inhibiting, respectively,
CC the expression or activity of basic transcription factor (BTF)3 or its
CC homologue in the cell. The BTF3 polypeptides and nucleic acids are useful
CC for inhibiting or increasing programmed cell death. They are used for
CC screening for an agent that increases or inhibits programmed cell death
CC or pre-screening for an agent that modulates programmed cell death. The
CC screened agent that increases or inhibits programmed cell death, is used
CC for diagnosing or treating cancer or neurodegenerative diseases (e.g.
CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease
CC or multiple sclerosis), atherosclerosis, or rheumatoid arthritis.
XX Sequences ABP71106-123 represent CARD regions of various CARD proteins
XX
SQ Sequence 10 AA;

Query Match 2.4%; Score 10; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 RDQARQLIID 61
|||||
Db 1 RDQARQLIID 10

RESULT 37
AAM68529
ID AAM68529 standard; protein; 163 AA.
XX

```
AC AAM68529;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human bone marrow expressed probe encoded protein SEQ ID NO: 28835.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma.
XX
XX Homo sapiens.
XX
XX WO200157276-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US0006568.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human bone marrow.
XX
XX Example 4; SEQ ID NO 28835; 658pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is a
XX protein encoded by one of the probes of the invention
XX
XX Sequence 163 AA;
XX
XX Query Match 2.4%; Score 10; DB 4; Length 163;
XX Best Local Similarity 100.0%; Pred. No. 0.32;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 278 KPRLFFIQAC 287
XX |||||
XX Db 84 KPRLFFIQAC 93
XX
XX RESULT 38
XX ABG38107
XX ID ABG38107 standard; peptide; 163 AA.
XX
XX AC ABG38107;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human peptide encoded by genome-derived single exon probe SEQ ID 27772.
XX
XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
XX Chronic obstructive pulmonary disease; interstitial lung disease;
XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;
XX pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX primary ciliary dyskinesia; pulmonary hypertension;
XX hyaline membrane disease.
```

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XX
XX Homo sapiens.
XX
XX WO200186003-A2.
XX
XX 15-NOV-2001.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples.
XX
XX Claim 27; SEQ ID NO 27772; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of probes
XX : the novel set of probes which hybridise at high stringency to a nucleic
XX acid expressed in the human lung; measuring gene expression in a sample
XX derived from human lung, comprising (a) contacting the array with a
XX collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of the
XX array; identifying exons in a eukaryotic genome, comprising (a)
XX algorithmically predicting at least one exon from genomic sequences of
XX the eukaryote; and (b) detecting specific hybridisation of detectably
XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX having a fragment identical to the predicted exon, the probe is included
XX in the above mentioned microarray; assigning exons to a single gene.
XX comprising (a) identifying exons from genomic sequence by the method
XX above and (b) measuring the expression of each of the exons in several
XX tissues and/or cell types using hybridisation to a single exon
XX microarrays having a probe with the exon, where a common pattern of
XX expression of the exons in the tissues and/or cell types indicates that
XX the exons should be assigned to a single gene; a peptide comprising one
XX of 12011 sequences, mentioned in the specification, or encoded by the
XX probes/open reading frames (ORF). The probes are used for gene expression
XX analysis, and for identifying exons in a gene, particularly using human
XX lung derived mRNA and for the study of lung diseases such as asthma, lung
XX cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
XX disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
XX tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
XX Pudlak syndrome, sarcoidosis, pulmonary haemorrhoidosis, pulmonary
XX histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
XX Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
XX dyskinesia, pulmonary hypertension and hyaline membrane disease. The
XX present sequence is a peptide/protein encoded by a single exon probe of
XX the invention. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIFO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 163 AA;
```

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Query Match 2.4%; Score 10; DB 5; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 278 KPCLFFIQAC 287
Db 84 KPCLFFIQAC 93

RESULT 39
AAB98655
ID AAB98655 standard; protein; 244 AA.
XX AC
XX AAB98655;
XX 16-AUG-2001 (first entry)
DT FT
XX Caspase-7.
DE FT
XX Caspase-1; Protein co-ordinate data; caspase-7; S4 binding region;
KW caspase-3.
XX Unidentified.
XX WO200137194-A2.
PN FT
XX 25-MAY-2001.
XX 16-NOV-2000; 2000WO-US031602.
PF FT
XX 16-NOV-1999; 99US-0165797P.
PR FT
XX (VERT-) VERTEX PHARM INC.
PA FT
XX Wei Y;
PI FT
XX WPI; 2001-329229/34.
DR FT
XX Molecule or molecular complex used for drug discovery, comprises a
PT binding pocket of caspase-7 or a homolog having an S4 binding region more
PT hydrophilic than that of caspase-3.
XX
XX Example 4; Fig 3; 161pp; English.
XX
XX The present invention relates to a molecule or molecular complex (1)
CC comprising a binding pocket defined by the structure coordinates of
CC caspase-7 amino acids 234, 235, 237, 276, 278, 281, and 284 or a homolog
CC of (1) with a binding pocket having a root mean square deviation from the
CC amino acid backbone atoms of not more than 1.5 Angstrom, where (1) has an
CC S4 binding region that is more hydrophilic than that of caspase-3. The
CC present sequence is caspase-7, which was used in a sequence homology
CC alignment
XX
XX SQ Sequence 244 AA;
XX
XX Query Match 2.4%; Score 10; DB 4; Length 244;
XX Best Local Similarity 100.0%; Pred. No. 0.46;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFIQAC 287
Db 118 KPCLFFIQAC 127

RESULT 40
AAB15262
ID AAB15262 standard; protein; 303 AA.
XX AC
XX AAB15262;
XX 05-AUG-1997 (first entry)
DT FT
XX Apoptotic protease Mch3-alpha.
DE FT
XX Mch3-alpha; cysteine protease; apoptosis; AIDS; ischaemia;
KW neurodegenerative disease; therapy; diagnosis.
XX
```

```
OS Homo sapiens.
XX Key
XX Domain
XX 1..198
XX /label= P20
XX /note= "p20 subunit"
XX 24..28
XX /label= P20
XX 54..58
XX /label= P17
XX 99..103
XX /label= P12
XX 184..188
XX /note= "QACRG active site"
XX 199..303
XX /label= P12
XX /note= "p12 subunit"
XX
XX WO9718313-A1.
XX
XX 22-MAY-1997.
XX
XX 12-NOV-1996; 96WO-US018118.
XX
XX 13-NOV-1995; 95US-00556627.
XX
XX (IDUN-) IDUN PHARM INC.
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES, Fernandes-Alnemri T, Litwack G, Armstrong R;
XX Tomaselli K;
XX WPI; 1997-289289/26.
XX N-PSDB; AAT66992.
XX
XX New gene encoding Mch3, a cysteine protease that regulates apoptosis -
XX for treating human diseases associated with apoptosis, and screening for
XX antagonists and agonists of Mch3.
XX
XX Claim 8; Fig 1; 52pp; English.
XX
XX Human Mch3-alpha (AAW15262) is an apoptotic protein and novel member of
XX the interleukin-1-beta converting enzyme (ICE) family of cysteine
XX proteases. Its amino acid sequence was deduced from a cDNA clone
XX (AAT66992) obt'd. from a Jurkat library. Mch3-beta (AAW15263) has also
XX been identified that lacks the active site of Mch3-alpha. Mch3-alpha
XX polypeptides can be produced in engineered host cells and used to treat
XX human diseases associated with cell death, such as AIDS, ischaemic
XX injury, neurodegenerative diseases, etc. They can also be used to
XX regulate apoptosis and to screen for Mch3 agonists and antagonists
XX
XX SQ Sequence 303 AA;
XX
XX Query Match 2.4%; Score 10; DB 2; Length 303;
XX Best Local Similarity 100.0%; Pred. No. 0.55;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFIQAC 287
Db 177 KPCLFFIQAC 186

RESULT 41
AAB15247
ID AAB15247 standard; protein; 303 AA.
XX AC
XX AAB15247;
XX 21-JUL-1997 (first entry)
DT FT
XX Cysteine protease CMH-1.
DE FT
XX Cysteine protease; CMH-1; CPP32/Mch2 homologue-1; apoptosis;
KW
```

KW programmed cell death; cancer; neurodegenerative disease;
 KW autoimmune disease; gene therapy; diagnosis.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= Pro-peptide
 FT Protein 24..303
 FT /label= Mat.protein
 FT /note= "active CMH-1 polypeptide (Claim 3)"
 FT Protein 29..303
 FT /label= Mat.protein
 FT /note= "active CMH-1 polypeptide (Claim 3)"
 FT Active-site 155
 FT /note= "His144 is a catalytic residue"
 FT Active-site 186
 FT /note= "Cys186 is a catalytic residue"
 XX
 PN WO9716552-A1.
 XX
 PD 09-MAY-1997.
 XX
 PD 01-NOV-1996; 96WO-US017431.
 XX
 PR 03-NOV-1995; 95US-0007211P.
 PR 06-NOV-1995; 95US-0007251P.
 PR 16-NOV-1995; 95US-00558733.
 XX
 PA (VERT-) VERTEX PHARM INC.
 XX
 PI Su M, Lippke JA;
 PI
 DR WPI: 1997-272121/24.
 DR N-PSDB; AA166970.
 XX
 PT DNA encoding active, activatable or inactive cysteine protease CMH-1 -
 PT useful in gene therapy for promoting and inhibiting apoptosis and for
 PT diagnosing cells with potential for apoptosis.
 XX
 PS Claim 3; Page 32-33; 48pp; English.
 XX
 CC A proenzyme (AAW15247) is activated to CMH-1, or CPP32/Mch2 homologue-1,
 CC a human cysteine protease that is involved in apoptosis. Its amino acid
 CC sequence was deduced from a full-length isolated cDNA clone (AA166970).
 CC Active, activatable (i.e. proenzyme) or inactivated forms of CMH-1 can be
 CC expressed in prokaryotic or eukaryotic host cells. The polypeptides are
 CC useful for screening potential apoptosis inhibitors and for raising
 CC antibodies used to assay CMH-1, to regulate cholesterol levels, inhibit
 CC CMH-1 activity and therefore apoptosis, and to purify CMH-1 polypeptides
 SQ Sequence 303 AA;

Query Match 2.4%; Score 10; DB 2; Length 303;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 278 KPFLFFIQAC 287
 |||||
 DB 177 KPFLFFIQAC 186

RESULT 42
 AAY21721
 ID AAY21721 standard; protein; 303 AA.
 XX
 AC AAY21721;
 XX
 DT 10-SEP-1999 (first entry)
 XX
 DE Amino acid sequence of caspase-7 (Mch3).
 XX
 KW Rev-caspase; cysteine protease; zymogen; cancer; gene therapy;

KW autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
 KW tumour cell; myocardial infarction; human.
 XX Homo sapiens.
 OS
 PN WO9935277-A2.
 XX
 PD 15-JUL-1999.
 XX
 PF 11-JAN-1999; 99WO-US000632.
 XX
 PR 09-JAN-1998; 98US-0070987P.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Alnemri ES;
 PI
 DR WPI: 1999-419353/35.
 DR N-PSDB; AAX81223.
 XX
 PT New isolated nucleic acid molecule encoding a rev-caspase - used for
 PT screening and identifying inhibitors or enhancers for treating cancer or
 PT autoimmune disease.
 XX
 PS Disclosure; Fig 17A-B; 74pp; English.
 XX
 CC The invention relates to nucleic acid molecules encoding rev-caspases.
 CC Rev-caspases are cysteine proteases that specifically cleave proteins
 CC after Asp residues and is expressed as a zymogen, in which the small
 CC subunit is N-terminal to a large subunit. A gene delivery vehicle
 CC comprising a rev-caspase coding sequence is useful for the treatment of
 CC cancer, where the gene delivery vehicle is internalised by tumour cells.
 CC The gene delivery vehicle can also be used to treat autoimmune diseases.
 CC Cells transfected with a rev-caspase expressing vector can be used in
 CC identification of inhibitors or enhancers of caspase-mediated apoptosis.
 CC In vitro translated rev-caspase can be used to identify an inhibitor or
 CC enhancer of caspase processing activity. Caspase inhibitors are useful
 CC for treating neurodegenerative diseases as well as for inhibiting
 CC apoptosis in the heart following myocardial infarction. Sequences
 CC AAX81217 -AAX81226 represent human caspase genes encoding caspase 1-10
 CC gene products (AAY21715-Y21724)
 XX
 SQ Sequence 303 AA;

Query Match 2.4%; Score 10; DB 2; Length 303;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 278 KPFLFFIQAC 287
 |||||
 DB 177 KPFLFFIQAC 186

RESULT 43
 AAE00604
 ID AAE00604 standard; protein; 303 AA.
 XX
 AC AAE00604;

DT 02-JUL-2001 (first entry)
 XX
 DE Human caspase-7.

KW Human; caspase-7; interleukin-1 converting enzyme; ICE-LAP3; CHM-1; Mch3;
 KW cysteine protease; apoptosis; caspase expression cassette; metastasis;
 KW tumour; cathepsin B; urokinase; proliferation; gene therapy.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Cleavage-site 23..24
 FT /label= Proteolytic_cleavage_site
 FT Cleavage-site 198..199

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FT Cleavage-site /label= Proteolytic_cleavage_site
FT 206..207
FT /label= Proteolytic_cleavage_site
XX
XX WO200129232-A2.
XX
XX 26-APR-2001.
XX
XX 19-OCT-2000; 2000WO-US028941.
XX
XX 20-OCT-1999; 99US-0160559P.
XX
XX 14-AUG-2000; 2000US-0225564P.
XX
XX (SCIO-) SCIOS INC.
XX
XX Cordell B, Li Y;
XX
XX WPI; 2001-290920/30.
XX
XX N-PSDB; AAD03914.
XX
XX Novel fusion polypeptide comprising first and second caspase subunit
XX separated by cleavage site not associated in nature with caspase subunit,
XX useful for cloning gene encoding enzymes involved in proteolytic
XX cleavage.
XX
XX Claim 4; Fig 14; 116pp; English.
XX
XX The present amino acid sequence is human Caspase-7 also known as
XX interleukin-1 converting enzyme (ICE) LAP3, CHM-1 and Mhc3. Caspases are
XX a family of cysteine proteases, that participate in the initiation and
XX execution of apoptosis. Caspases exist as pro-enzymes, activated by
XX cleavage into a large and small subunit, occurring after specific
XX aspartic acid residues within the pro-enzyme sequence. The present
XX invention relates to a method for functional cloning of genes encoding
XX proteins or enzymes involved in proteolytic cleavage. The invention is
XX based on the use of caspase expression cassettes comprising the coding
XX sequence of a proteolytic cleavage site flanked by sequences encoding two
XX caspase subunits. A fusion polypeptide comprising a first and a second
XX caspase subunit, separated by a cleavage site not associated in nature,
XX is useful for cloning gene encoding enzymes involved in proteolytic
XX cleavage. An expression cassette containing fusion polypeptide is used to
XX identify a mutant cell line deficient in an enzyme of interest and is
XX also useful for diagnosis and suppression of proliferation or metastases
XX of a tumour cell characterised by overexpression of a polypeptide (e.g.
XX Cathepsin B or urokinase, selectively expressed in the tumour cells). DNA
XX encoding fusion polypeptide is used in gene therapy
XX
XX Sequence 303 AA;
XX
XX Query Match 2.4%; Score 10; DB 4; Length 303;
XX Best Local Similarity 100.0%; Pred. No. 0.55; Indels 0; Gaps 0;
XX Matches 10; Conservative 0; Mismatches 0;
XX
XX QY 278 KPKLFFFIQAC 287
XX |||||
XX Db 177 KPKLFFFIQAC 186
XX
XX RESULT 44
XX ABJ01222
XX ID ABJ01222 standard; protein; 303 AA.
XX
XX AC ABJ01222;
XX
XX 18-SEP-2002 (first entry)
XX
XX Human caspase-7 SEQ ID NO: 24.
XX
XX Human; caspase; rev-caspase; gene therapy; protease; apoptosis; cancer;
XX autoimmune disease; cytostatic; immunosuppressive.
XX
XX Homo sapiens.
XX
XX
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```
PN US6376226-B1.
XX
XX 23-APR-2002.
XX
XX 26-APR-2000; 2000US-00561756.
XX
XX 09-JAN-1998; 98US-0070897P.
XX
XX 08-JAN-1999; 99US-00227721.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 2002-453146/48.
XX
XX N-PSDB; ABT03970.
XX
XX New rev-caspases engineered to contain the small subunit fused in frame N
XX -terminal to the large subunit, which is in reverse order to the wild
XX type caspases, are useful to treat cancer and autoimmune diseases.
XX
XX Disclosure; Fig 17; 81pp; English.
XX
XX The present invention provides the protein and coding sequences of human
XX rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences
XX can be used in the gene therapy of cancer and autoimmune diseases. The
XX present sequence is a protein described in the exemplification of the
XX invention
XX
XX Sequence 303 AA;
XX
XX Query Match 2.4%; Score 10; DB 5; Length 303;
XX Best Local Similarity 100.0%; Pred. No. 0.55; Indels 0; Gaps 0;
XX Matches 10; Conservative 0; Mismatches 0;
XX
XX QY 278 KPKLFFFIQAC 287
XX |||||
XX Db 177 KPKLFFFIQAC 186
XX
XX RESULT 45
XX ABB78588
XX ID ABB78588 standard; protein; 303 AA.
XX
XX AC ABB78588;
XX
XX 15-JUL-2002 (first entry)
XX
XX Mouse caspase 7 protein sequence SEQ ID NO:97.
XX
XX Caspase 7; antisense modulation; antiinflammatory; cytostatic;
XX antisense therapy; caspase 7 inhibitor; inflammatory condition;
XX hyperproliferative disorder; cancer; bone metabolism; infection;
XX cholesterol disorder; inflammation; tumour.
XX
XX Mus musculus.
XX
XX WO200222640-A1.
XX
XX 21-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US028232.
XX
XX 11-SEP-2000; 2000US-00659860.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Zhang H, Watt AT;
XX
XX WPI; 2002-404806/43.
XX
XX N-PSDB; ABN80919.
XX
XX Novel antisense compounds targeted to nucleic acids encoding caspase 7,
XX for modulating gene expression and treating diseases associated with
XX
```

PT	expression of caspase 7 in humans.
PS	Example 16; Page 121-123; 138pp; English.
XX	The present invention describes a compound (I) 8-50 nucleobases in length targeted to a nucleic acid molecule encoding caspase 7, which specifically hybridises with and inhibits the expression of caspase 7. (I) has antiinflammatory and cytostatic activities, and can be used in antisense therapy and as an inhibitor of caspase 7 expression. (I) is useful for inhibiting the expression of caspase 7 in human cells or tissues, and for treating a human having a disease or condition associated with caspase 7 including inflammatory condition, hyperproliferative disorder (cancer), or bone metabolism or cholesterol disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and as research reagent and kits. (I) is useful prophylactically to prevent or delay infection, inflammation or tumour formation. The present sequence represents a mouse caspase 7 protein, which is used in an example from the present invention
CC	Query Match 2.4%; Score 10; DB 5; Length 303;
CC	Best Local Similarity 100.0%; Pred. No. 0.55;
CC	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	278 KPKLFFFIQAC 287
DB	177 KPKLFFFIQAC 186
RESULT 46	
ABB09299	
ID	ABB09299 standard; protein; 303 AA.
XX	
AC	ABB09299;
XX	
DT	15-JUL-2002 (first entry)
XX	
DE	Human caspase 7 protein sequence SEQ ID NO:17.
XX	
KW	Caspase 7; antisense modulation; antiinflammatory; cytostatic; antisense therapy; caspase 7 inhibitor; inflammatory condition; hyperproliferative disorder; cancer; bone metabolism; infection; cholesterol disorder; inflammation; tumour.
KW	
KW	
KW	
OS	Homo sapiens.
XX	
PN	WO200222640-A1.
XX	
PD	21-MAR-2002.
XX	
PF	10-SEP-2001; 2001WO-US028232.
FR	
XX	
PR	11-SEP-2000; 2000US-00659860.
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
PI	Zhang H, Watt AT;
XX	
DR	WPI; 2002-404806/43.
N-PSDB; ABN80839.	
XX	
PT	Novel antisense compounds targeted to nucleic acids encoding caspase 7, for modulating gene expression and treating diseases associated with expression of caspase 7 in humans.
XX	
PS	Example 15; Page 101-103; 138pp; English.
XX	
CC	The present invention describes a compound (I) 8-50 nucleobases in length targeted to a nucleic acid molecule encoding caspase 7, which specifically hybridises with and inhibits the expression of caspase 7. (I) has antiinflammatory and cytostatic activities, and can be used in antisense therapy and as an inhibitor of caspase 7 expression. (I) is useful for inhibiting the expression of caspase 7 in human cells or tissues, and for treating a human having a disease or condition associated with caspase 7 including inflammatory condition, hyperproliferative disorder (cancer), or bone metabolism or cholesterol disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and as research reagent and kits. (I) is useful prophylactically to prevent or delay infection, inflammation or tumour formation. The present sequence represents a mouse caspase 7 protein, which is used in an example from the present invention
CC	Query Match 2.4%; Score 10; DB 5; Length 303;
CC	Best Local Similarity 100.0%; Pred. No. 0.55;
CC	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	278 KPKLFFFIQAC 287
DB	177 KPKLFFFIQAC 186
RESULT 46	
ABB09299	
ID	ABB09299 standard; protein; 303 AA.
XX	
AC	ABB09299;
XX	
DT	15-JUL-2002 (first entry)
XX	
DE	Human caspase 7 protein sequence SEQ ID NO:17.
XX	
KW	Caspase 7; antisense modulation; antiinflammatory; cytostatic; antisense therapy; caspase 7 inhibitor; inflammatory condition; hyperproliferative disorder; cancer; bone metabolism; infection; cholesterol disorder; inflammation; tumour.
KW	
KW	
KW	
OS	Homo sapiens.
XX	
PN	WO200222640-A1.
XX	
PD	21-MAR-2002.
XX	
PF	10-SEP-2001; 2001WO-US028232.
FR	
XX	
PR	11-SEP-2000; 2000US-00659860.
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
PI	Zhang H, Watt AT;
XX	
DR	WPI; 2002-404806/43.
N-PSDB; ABN80839.	
XX	
PT	Novel antisense compounds targeted to nucleic acids encoding caspase 7, for modulating gene expression and treating diseases associated with expression of caspase 7 in humans.
XX	
PS	Example 15; Page 101-103; 138pp; English.
XX	
CC	The present invention describes a compound (I) 8-50 nucleobases in length targeted to a nucleic acid molecule encoding caspase 7, which specifically hybridises with and inhibits the expression of caspase 7. (I) has antiinflammatory and cytostatic activities, and can be used in antisense therapy and as an inhibitor of caspase 7 expression. (I) is useful for inhibiting the expression of caspase 7 in human cells or tissues, and for treating a human having a disease or condition associated with caspase 7 including inflammatory condition, hyperproliferative disorder (cancer), or bone metabolism or cholesterol disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and as research reagent and kits. (I) is useful prophylactically to prevent or delay infection, inflammation or tumour formation. The present sequence represents a mouse caspase 7 protein, which is used in an example from the present invention
CC	Query Match 2.4%; Score 10; DB 5; Length 303;
CC	Best Local Similarity 100.0%; Pred. No. 0.55;
CC	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	278 KPKLFFFIQAC 287
DB	177 KPKLFFFIQAC 186
RESULT 47	
ABB09297	
ID	ABB09297 standard; protein; 303 AA.
XX	
AC	ABB09297;
XX	
DT	15-JUL-2002 (first entry)
XX	
DE	Human caspase 7 protein sequence SEQ ID NO:3.
XX	
KW	Caspase 7; antisense modulation; antiinflammatory; cytostatic; antisense therapy; caspase 7 inhibitor; inflammatory condition; hyperproliferative disorder; cancer; bone metabolism; infection; cholesterol disorder; inflammation; tumour.
KW	
KW	
KW	
OS	Homo sapiens.
XX	
PN	WO200222640-A1.
XX	
PD	21-MAR-2002.
XX	
PF	10-SEP-2001; 2001WO-US028232.
FR	
XX	
PR	11-SEP-2000; 2000US-00659860.
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
PI	Zhang H, Watt AT;
XX	
DR	WPI; 2002-404806/43.
N-PSDB; ABN80825.	
XX	
PT	Novel antisense compounds targeted to nucleic acids encoding caspase 7, for modulating gene expression and treating diseases associated with expression of caspase 7 in humans.
XX	
PS	Example 13; Page 94-96; 138pp; English.
XX	
CC	The present invention describes a compound (I) 8-50 nucleobases in length targeted to a nucleic acid molecule encoding caspase 7, which specifically hybridises with and inhibits the expression of caspase 7. (I) has antiinflammatory and cytostatic activities, and can be used in antisense therapy and as an inhibitor of caspase 7 expression. (I) is useful for inhibiting the expression of caspase 7 in human cells or tissues, and for treating a human having a disease or condition associated with caspase 7 including inflammatory condition, hyperproliferative disorder (cancer), or bone metabolism or cholesterol disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and as research reagent and kits. (I) is useful prophylactically to prevent or delay infection, inflammation or tumour formation. The present sequence represents a human caspase 7 protein, which is used in an example from the present invention
CC	Query Match 2.4%; Score 10; DB 5; Length 303;
CC	Best Local Similarity 100.0%; Pred. No. 0.55;
CC	Matches 10;

XX SQ Sequence 303 AA;
Query Match 2.4%; Score 10; DB 5; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 278 KPKLFFFIQAC 287
Db 177 KPKLFFFIQAC 186
RESULT 48
AAO19868
ID AAO19868 standard; protein; 303 AA.
XX AC AAO19868;
XX DT 11-AUG-2003 (first entry)
XX DE Bacteriophage caspase 7 protein.
XX KW Bacteriophage; lytic; pathogenic bacterium; phage; annihilation moiety;
KW infection; tuberculosis; AIDS; HIV infection; malaria; mutagenic;
KW tuberculostatic; anti-HIV; virucide; protozoacide; antibacterial.
XX OS Bacteriophage.
XX PN WO2003000274-A2.
XX PD 03-JAN-2003.
XX PF 21-JUN-2002; 2002WO-GB002879.
XX PR 22-JUN-2001; 2001GB-00015385.
XX PA (REGM-) REGMA BIO TECHNOLOGIES LTD.
XX PA (POLY/) POLYANSKAYA N.
XX PI Pasechnik V, West D;
XX WPI; 2003-210119/20.
XX DR N-PSDB; ABZ69367.
PT Bacteriophage preparation for stimulating death of infected cell, has
PT bacteriophage that enters cell and lyses pathogenic bacteria that infect
PT cells, linked to annihilation moiety that stimulates death of infected
PT cells.
XX PS Disclosure; Page 21; 45pp; English.
XX CC The present invention relates to a bacteriophage preparation, comprising
CC a bacteriophage modified to enter eukaryotic cells, which is lytic to
CC pathogenic bacterial strain infecting the cell, and is capable of
CC expressing an annihilation moiety. Said moiety will then cause the death
CC or inactivation of an infected cell. In particular, the preparation can
CC be used to kill cells infected with tuberculosis, HIV, AIDS and malaria.
CC The present sequence is a protein produced by a DNA fragment used to
CC produce the modified bacteriophage of the invention
XX SQ Sequence 303 AA;
Query Match 2.4%; Score 10; DB 6; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 278 KPKLFFFIQAC 287
Db 177 KPKLFFFIQAC 186
RESULT 49
ABB69920
ID ABB69920 standard; protein; 308 AA.
XX AC ABB69920;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 36552.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX DR N-PSDB; ABL14023.
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX PS Disclosure; SEQ ID NO 36552; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 308 AA;
Query Match 2.4%; Score 10; DB 4; Length 308;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 278 KPKLFFFIQAC 287
Db 162 KPKLFFFIQAC 171
RESULT 50
ABB09300
ID ABB09300 standard; protein; 336 AA.
XX AC ABB09300;
XX DT 15-JUL-2002 (first entry)
XX DE Human caspase 7 protein sequence SEQ ID NO:18.
XX KW Caspase 7; antisense modulation; antiinflammatory; cytostatic;
KW antisense therapy; caspase 7 inhibitor; inflammatory condition;
KW hyperproliferative disorder; cancer; bone metabolism; infection;
KW cholesterol disorder; inflammation; tumour.
XX OS Homo sapiens.

XX SQ Sequence 303 AA;
Query Match 2.4%; Score 10; DB 5; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 278 KPKLFFFIQAC 287
Db 177 KPKLFFFIQAC 186
RESULT 48
AAO19868
ID AAO19868 standard; protein; 303 AA.
XX AC AAO19868;
XX DT 11-AUG-2003 (first entry)
XX DE Bacteriophage caspase 7 protein.
XX KW Bacteriophage; lytic; pathogenic bacterium; phage; annihilation moiety;
KW infection; tuberculosis; AIDS; HIV infection; malaria; mutagenic;
KW tuberculostatic; anti-HIV; virucide; protozoacide; antibacterial.
XX OS Bacteriophage.
XX PN WO2003000274-A2.
XX PD 03-JAN-2003.
XX PF 21-JUN-2002; 2002WO-GB002879.
XX PR 22-JUN-2001; 2001GB-00015385.
XX PA (REGM-) REGMA BIO TECHNOLOGIES LTD.
XX PA (POLY/) POLYANSKAYA N.
XX PI Pasechnik V, West D;
XX WPI; 2003-210119/20.
XX DR N-PSDB; ABZ69367.
PT Bacteriophage preparation for stimulating death of infected cell, has
PT bacteriophage that enters cell and lyses pathogenic bacteria that infect
PT cells, linked to annihilation moiety that stimulates death of infected
PT cells.
XX PS Disclosure; Page 21; 45pp; English.
XX CC The present invention relates to a bacteriophage preparation, comprising
CC a bacteriophage modified to enter eukaryotic cells, which is lytic to
CC pathogenic bacterial strain infecting the cell, and is capable of
CC expressing an annihilation moiety. Said moiety will then cause the death
CC or inactivation of an infected cell. In particular, the preparation can
CC be used to kill cells infected with tuberculosis, HIV, AIDS and malaria.
CC The present sequence is a protein produced by a DNA fragment used to
CC produce the modified bacteriophage of the invention
XX SQ Sequence 303 AA;
Query Match 2.4%; Score 10; DB 6; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 278 KPKLFFFIQAC 287
Db 177 KPKLFFFIQAC 186
RESULT 49
ABB69920
ID ABB69920 standard; protein; 308 AA.
XX AC ABB69920;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 36552.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX DR N-PSDB; ABL14023.
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX PS Disclosure; SEQ ID NO 36552; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 308 AA;
Query Match 2.4%; Score 10; DB 4; Length 308;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 278 KPKLFFFIQAC 287
Db 162 KPKLFFFIQAC 171
RESULT 50
ABB09300
ID ABB09300 standard; protein; 336 AA.
XX AC ABB09300;
XX DT 15-JUL-2002 (first entry)
XX DE Human caspase 7 protein sequence SEQ ID NO:18.
XX KW Caspase 7; antisense modulation; antiinflammatory; cytostatic;
KW antisense therapy; caspase 7 inhibitor; inflammatory condition;
KW hyperproliferative disorder; cancer; bone metabolism; infection;
KW cholesterol disorder; inflammation; tumour.
XX OS Homo sapiens.


```
XX WO200222640-A1.
PN
XX
XX 21-MAR-2002.
PD
XX
XX 10-SEP-2001; 2001WO-US028232.
PF
XX
XX 11-SEP-2000; 2000US-00659860.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Zhang H, Watt AT;
PI
XX
XX WPI; 2002-404806/43.
DR
XX
XX N-PSDB; ABN80840.
DR
XX
XX Novel antisense compounds targeted to nucleic acids encoding caspase 7,
PT for modulating gene expression and treating diseases associated with
PT expression of caspase 7 in humans.
PT
XX
XX Example 15; Page 103-105; 138pp; English.
PS
XX
XX The present invention describes a compound (I) 8-50 nucleobases in length
CC targeted to a nucleic acid molecule encoding caspase 7, which
CC specifically hybridizes with and inhibits the expression of caspase 7.
CC (I) has antinflammatory and cytostatic activities, and can be used in
CC antisense therapy and as an inhibitor of caspase 7 expression. (I) is
CC useful for inhibiting the expression of caspase 7 in human cells or
CC tissues, and for treating a human having a disease or condition
CC associated with caspase 7 including inflammatory condition,
CC hyperproliferative disorder (cancer), or bone metabolism or cholesterol
CC disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and as
CC research reagent and kits. (I) is useful prophylactically to prevent or
CC delay infection, inflammation or tumour formation. The present sequence
CC represents a human caspase 7 protein, which is used in an example from
CC the present invention
XX
XX Sequence 336 AA;
SQ
Query Match 2.4%; Score 10; DB 5; Length 336;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 278 KPKLFFIQAC 287
Db 210 KPKLFFIQAC 219
|||||
|||||
Search completed: August 3, 2004, 09:09:29
Job time : 57 secs
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OM protein - protein search, using sw model

Run on: August 3, 2004, 09:03:42 ; Search time 13 Seconds
(without alignments)

1666.245 Million cell updates/sec

Title: US-09-961-201A-1

Perfect score: 416

Sequence: 1 MDEADRLRLRRCLRLVEEL.....YKQMGCFNLRKLFKFKTS 416

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	219	52.6	416	1	ICE9_HUMAN
2	11	2.6	299	1	ICE1_SPOFR
3	11	2.6	333	1	ICE1_DROME
4	11	2.6	339	1	ICE1_DROME
5	10	2.4	303	1	ICE7_HUMAN
6	10	2.4	303	1	ICE7_HUMAN
7	10	2.4	303	1	ICE7_MOUSE
8	10	2.4	521	1	ICEA_HUMAN
9	9	2.2	484	1	CFLA_MOUSE
10	9	2.2	1196	1	BR11_ARATH
11	8	1.9	232	1	YK10_ARCFU
12	8	1.9	579	1	Y876_MYCLE
13	8	1.9	1207	1	BR11_LYCEP
14	8	1.9	1207	1	BR11_LYCEP
15	8	1.9	1393	1	RPOC_CHLNP
16	7	1.7	132	1	GC5H_MYCLE
17	7	1.7	180	1	PTH_CHLNP
18	7	1.7	196	1	HNK2_XENLA
19	7	1.7	210	1	GIDB_RHIL0
20	7	1.7	264	1	RS3_RALSO
21	7	1.7	274	1	NHS_STRAS
22	7	1.7	306	1	SDBS_PSES9
23	7	1.7	338	1	G3P_THEVO
24	7	1.7	345	1	TRPD_AERPE
25	7	1.7	349	1	TRUD_SALTI
26	7	1.7	349	1	TRUD_SALTI
27	7	1.7	401	1	RAY1_YEAST
28	7	1.7	404	1	YBR3_YEAST
29	7	1.7	420	1	BACA_RHIME
30	7	1.7	426	1	LIP7_CANAL
31	7	1.7	437	1	RECA_TROWT
32	7	1.7	442	1	IFR2_HUMAN
33	7	1.7	480	1	ICE8_MOUSE

34	7	1.7	487	1	PHOQ_SALTY
35	7	1.7	503	1	VRK2_MOUSE
36	7	1.7	504	1	PSD5_HUMAN
37	7	1.7	505	1	SPKD_SYNY3
38	7	1.7	508	1	VRK2_HUMAN
39	7	1.7	548	1	SYK_HALN1
40	7	1.7	551	1	E2K2_HUMAN
41	7	1.7	575	1	GGT_PSESP
42	7	1.7	628	1	LJ_HUMAN
43	7	1.7	664	1	UL47_HSVLP
44	7	1.7	749	1	TR2M_AGRRH
45	7	1.7	755	1	TR2M_AGR74
46	7	1.7	755	1	TR2N_AGRVI
47	7	1.7	778	1	YQ34_MYCTU
48	7	1.7	805	1	HIFA_XENLA
49	7	1.7	1011	1	CAPP_SYNEL
50	7	1.7	1062	1	UL70_HCMVA
51	7	1.7	1507	1	Y056_HUMAN
52	7	1.7	1997	1	OTOF_HUMAN
53	7	1.7	3119	1	CA1C_MOUSE
54	7	1.7	3259	1	G0B1_HUMAN
55	6	1.4	45	1	ATI2_HSVB4
56	6	1.4	67	1	G0N1_MACMU
57	6	1.4	71	1	YQKK_BACSU
58	6	1.4	84	1	NTXP_TITSE
59	6	1.4	84	1	SCX7_TITSE
60	6	1.4	84	1	SCX7_TITSE
61	6	1.4	84	1	SCX7_TITSE
62	6	1.4	87	1	Y32A_MYCGE
63	6	1.4	89	1	SLTB_BPH30
64	6	1.4	90	1	G0N1_MOUSE
65	6	1.4	91	1	G0N1_PIG
66	6	1.4	92	1	G0N1_CAVPO
67	6	1.4	92	1	G0N1_HUMAN
68	6	1.4	92	1	G0N1_TUPGB
69	6	1.4	95	1	IHF8_RHOCA
70	6	1.4	97	1	PY_DICLA
71	6	1.4	98	1	ACYO_HUMAN
72	6	1.4	98	1	ACYO_MOUSE
73	6	1.4	100	1	ACYO_PIG
74	6	1.4	104	1	RS17_THETH
75	6	1.4	110	1	ETS2_LYTVA

ALIGNMENTS

RESULT 1
ICE9_HUMAN STANDARD; PRT: 416 AA.
AC P55211; O95348; Q2852; Q9B062; Q9UEQ3; Q9ULV8;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-9 precursor (BC 3.4.22.-) (CASP-9) (ICE-like apoptotic
protease 6) (ICE-LAP6) (Apoptotic protease Mch-6) (Apoptotic protease
activating factor 3) (APAF-3).
GN CASP9 OR MCH6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS VAL-28 AND ARG-221.
RX MEDLINE=96279246; PubMed=8663294;
RA Duan H., Orth K., Chinnaiyan A.M., Poirier G.G., Froelich C.J.,
He W.-W., Dixit V.M.;
RT ~~ICE-LAP6~~, a novel member of the ICE/Ced-3 gene family, is activated
by the cytotoxic T cell protease granzyme B;
RL J. Biol. Chem. 271:16720-16724 (1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND PROCESSING.
RC TISSUE=T-cell;

RX MEDLINE=97059171; PubMed=8900201;
 RA Srinivasula S.M., Fernandes-Alnemri T., Zangrilli J., Robertson N.,
 RA Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,
 RA Alnemri E.S.;
 RT "The Ced-3/interleukin 1beta converting enzyme-like homolog Mch6 and
 RT the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic
 RT mediator CPP32.";
 RL J. Biol. Chem. 271:27099-27106(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=99315341; PubMed=10384055;
 RA Hadano S., Kasir J., Nichol K., Rasper D.M., Vaillancourt J.P.,
 RA Sherer S.W., Beatty B.G., Ikeda J.E., Nicholson D.W., Hayden M.R.;
 RT "Genomic organization of the human caspase-9 gene on chromosome
 RT 1p36.1-p36.3.";
 RL Mamm. Genome 10:757-760(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=99168502; PubMed=10070954;
 RA Srinivasula S.M., Ahmad M., Guo Y., Zhan Y., Lazebnik Y.,
 RA Fernandes-Alnemri T., Alnemri E.S.;
 RT "Identification of an endogenous dominant-negative short isoform of
 RT caspase-9 that can regulate apoptosis.";
 RL Cancer Res. 59:999-1002(1999).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=99107856; PubMed=9890966;
 RA Seol D.W., Billiar T.R.;
 RT "A novel splicing product of human caspase-9 lacking protease
 RT activity.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANT VAL-28.
 RX MEDLINE=99107856; PubMed=9890966;
 RA Seol D.W., Billiar T.R.;
 RT "A caspase-9 variant missing the catalytic site is an endogenous
 RT inhibitor of apoptosis.";
 RL J. Biol. Chem. 274:2072-2076(1999).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS VAL-28; LEU-99; ILE-102;
 RP VAL-106; ASP-114; HIS-173 AND ARG-221.
 RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Thomas D.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marston H., Farmer A.A., Rubin G.M., Hong L.,
 RA Dapkin M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. Binding of caspase-9 to Apaf-
 CC 1 leads to activation of the protease which then cleaves and
 CC activates caspase-3. Proteolytically cleaves poly(ADP-ribose)
 CC polymerase (PARP).
 CC -!- FUNCTION: Isoform 2 lacks activity is an dominant-negative
 CC inhibitor of caspase-9.
 CC -!- SUBUNIT: Heterodimer of a 35 kDa (p35) and a 10 kDa (p10) subunit.
 CC Caspase-9 and APAF1 bind to each other via their respective NH2-
 CC terminal CED-3 homologous domains in the presence of cytochrome C
 CC and ATP. Interacts with BIRC7.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=9L, Alpha;
 CC IsoId=P55211-1; Sequence=displayed;
 CC Name=2; Synonyms=9S, Beta;
 CC IsoId=P55211-2; Sequence=VSP_000818;
 CC -!- TISSUE SPECIFICITY: Ubiquitous, with highest expression in the
 CC heart, moderate expression in liver, skeletal muscle, and
 CC pancreas. Low levels in all other tissues.
 CC -!- PTM: CLEAVAGES AT ASP-315 BY GRANZYME B AND AT ASP-330 BY CPP32
 CC INVOLVED IN THESE PROCESSING EVENTS.
 CC -!- SIMILARITY: Belongs to peptidase family C14.
 CC -!- SIMILARITY: Contains 1 CARD domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch.

DR EMBL; U56390; AAC50640.1; -
 DR EMBL; U60521; AAC50776.1; -
 DR EMBL; AB019205; BAA82697.1; JOINED.
 DR EMBL; AB019197; BAA82697.1; JOINED.
 DR EMBL; AB019198; BAA82697.1; JOINED.
 DR EMBL; AB019199; BAA82697.1; JOINED.
 DR EMBL; AB019200; BAA82697.1; JOINED.
 DR EMBL; AB019201; BAA82697.1; JOINED.
 DR EMBL; AB019202; BAA82697.1; JOINED.
 DR EMBL; AB019203; BAA82697.1; JOINED.
 DR EMBL; AB019204; BAA82697.1; JOINED.
 DR EMBL; AF093130; AAD12248.1; -
 DR EMBL; AB015553; BAA78780.1; -
 DR EMBL; AB020979; BAA87905.1; -
 DR EMBL; AF110376; RAD13615.1; -
 DR EMBL; AL512883; CAC42423.1; -
 DR EMBL; AY214168; AAO21133.1; -
 DR EMBL; BC002452; AAH02452.1; -
 DR EMBL; BC006463; AAH06463.1; -
 DR PDB; 3YGS; 19-APR-00.
 DR MEROPS; C14.010; -
 DR Genew; HGNC:1511; CASP9.
 DR MIM; 602334; -
 DR GO; GO:0004211; F:caspase-9 activity; TAS.
 DR GO; GO:0004197; F:cysteine-type endopeptidase activity; TAS.
 DR GO; GO:0008047; F:enzyme activator activity; TAS.
 DR GO; GO:0008233; F:peptidase activity; TAS.
 DR GO; GO:0008635; P:apoptotic program; TAS.
 DR GO; GO:0008315; P:caspase activation via cytochrome c; TAS.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR InterPro; IPR002398; Peptidase_C14.

```

DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis; Alternative splicing;
KW Polymorphism; 3D-structure.
FT CHAIN ? 315
FT PROPEP 316 330
FT CHAIN 331 416
FT DOMAIN 1 92
FT ACT_SITE 237 237
FT ACT_SITE 287 287
FT VARSPLIC 140 289
FT VARIANT 28 28
FT VARIANT 99 99
FT VARIANT 102 102
FT VARIANT 106 106
FT VARIANT 114 114
Query Match 52.6%; Score 219; DB 1; Length 416;
Best Local Similarity 99.7%; Pred. No. 2.4e-215;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 97 KLSKPTLENTPVVLREIKPEVLRPEPRPDVIGSGFGDVGALSLRGADLAYILS 156
Db 97 KLSKPTLENTPVVLREIKPEVLRPEPRPDVIGSGFGDVGALSLRGADLAYILS 156
QY 157 MFCGHCILINNVNFCRESGLRTGSDNIDCEKLRFRFSLHFMVEVKGDLTAKWVLAL 216
Db 157 MFCGHCILINNVNFCRESGLRTGSDNIDCEKLRFRFSLHFMVEVKGDLTAKWVLAL 216
QY 217 LELAQDHGALDCVVVILSHGQASHLPFGAVGTGDCPVSEKIVNFNGTSCPSLG 276
Db 217 LELAQDHGALDCVVVILSHGQASHLPFGAVGTGDCPVSEKIVNFNGTSCPSLG 276
QY 277 GKPLFFIOACGGEQKHGFVASTSPDESPGSPNPEPDATPFQEGRLTFDQLDAISSLP 336
Db 277 GKPLFFIOACGGEQKHGFVASTSPDESPGSPNPEPDATPFQEGRLTFDQLDAISSLP 336
QY 337 TFSDFVSYSTPFGVSWRDPKSGSWYVETLDDIFQWASHEDLQSLLRVANAVSKGI 396
Db 337 TFSDFVSYSTPFGVSWRDPKSGSWYVETLDDIFQWASHEDLQSLLRVANAVSKGI 396
QY 397 YKQMPGCFNFKKIFFKTS 416
Db 397 YKQMPGCFNFKKIFFKTS 416

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RESULT 2

```

ID ICEL SPOFR STANDARD; PRT; 299 AA.
AC P89116;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-1 precursor (EC 3.4.22.-)
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Amphipyrinae; Spodoptera.
OX NCBI_TaxID=7108;

```

```

RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97153084; PubMed=8999805;
RA Ahmad M., Srinivasula S.M., Wang L., Litwack G., Fernandes-Alnemri T.,
RA Alnemri E.S.;
RT "Spodoptera frugiperda caspase-1, a novel insect death protease that
RT cleaves the nuclear immunophilin FKBP46, is the target of the
RT baculovirus antiapoptotic protein p35.";
RL J. Biol. Chem. 272:1421-1424(1997).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution (By similarity). Inhibited by
CC the baculovirus anti-apoptotic protein p35. Cleaves p35 and
CC nuclear immunophilin FKBP46.
CC -!- SUBUNIT: Heterodimer of a 19/18 kDa (p19/18) and a 12 kDa (p12)
CC subunit.
CC -!- PTM: AN AUTOCATALYTIC MECHANISM GENERATES THE TWO ACTIVE SUBUNITS.
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U81510; AAC47442.1; -.
CC HSPP; P42574; ICP3.
CC MEROPS; C14.015; -.
CC InterPro; IPR002138; ICE_p10.
CC InterPro; IPR001309; ICE_p20.
CC InterPro; IPR002398; Peptidase C14.
CC Pfam; PF00656; Peptidase C14; 1.
CC PRINTS; PR00376; IL1BCENZYM.
CC SMART; SM00115; CASC; 1.
CC PROSITE; PS01122; CASPASE_CYS; 1.
CC PROSITE; PS01121; CASPASE_HIS; 1.
CC PROSITE; PS0207; CASPASE_P10; 1.
CC PROSITE; PS0208; CASPASE_P20; 1.
CC Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 28
FT CHAIN 29 184 CASPASE-1 SUBUNIT P19/18.
FT PROPEP 185 195 POTENTIAL.
FT CHAIN 196 299 CASPASE-1 SUBUNIT P12.
FT ACT_SITE 136 136 BY SIMILARITY.
FT ACT_SITE 178 178 BY SIMILARITY.
SQ SEQUENCE 299 AA; 33527 MW; 99F4FED09B04EEDC CRC64;
Query Match 2.6%; Score 11; DB 1; Length 299;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 277 GKPLFFIOAC 287
Db 168 GKPLFFIOAC 178

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RESULT 3

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ID ICEL DROME STANDARD; PRT; 323 AA.
AC O02002; Q9W1N0;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-1 precursor (EC 3.4.22.-)
GN DCP-1 OR C6370.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 216-248.

```

-1- SIMILARITY: Belongs to peptidase family C14.
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EMBL; AF001464; AAB58237.1; -;
 EMBL; AE003461; AAF47027.1; -;
 EMBL; BT010065; AAQ22534.1; -;
 HSSP; P42574; 1PAU.
 MEROPS; C14.016;
 Flybase; FBgn0010501; Dcp-1.
 GO; GO:0004199; F:caspace activity; IDA.
 GO; GO:0004207; F:effector caspase activity; NAS.
 GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; IMP.
 GO; GO:0008632; P:apoptotic program; IDA.
 GO; GO:0006922; P:cleavage of lamin; IMP.
 GO; GO:0009795; P:embryonic morphogenesis; IMP.
 GO; GO:0007300; P:nurse cell/oocyte transport (sensu Insecta); IMP.
 InterPro; IPR002138; ICE p10.
 InterPro; IPR001309; ICE p20.
 InterPro; IPR002398; Peptidase_C14.
 Pfam; PF00656; Peptidase_C14; 1.
 PRINTS; PR00376; ILRCENZYM.
 SMART; SM00115; CASC.1
 PROSITE; PS01122; CASPACE_CYS; 1.
 PROSITE; PS01121; CASPACE_HIS; 1.
 PROSITE; PS02007; CASPACE_P10; 1.
 PROSITE; PS02008; CASPACE_P20; 1.
 Hydrolase; Thiol protease; Zymogen; Apoptosis.
 PROPEP 1 33 PROBABLE
 CHAIN 34 202 CASPACE-1 SUBUNIT P22.
 PROPEP 203 215 CASPACE-1 SUBUNIT P13.
 CHAIN 216 323 BY SIMILARITY.
 ACT_SITE 154 154 BY SIMILARITY.
 ACT_SITE 196 196 BY SIMILARITY.
 SEQUENCE 323 AA; 35926 MW; B5FF0FF75EB8E2BD CRC64;

Query Match 2.6%; Score 11; DB 1; Length 323;
 Best Local similarity 100.0%; Pred. No. 0.0043;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 277 GKPKLFFIQAC 287
 DB 186 GKPKLFFIQAC 196

RESULT 4
 ICE_DROME STANDARD; PRT; 339 AA.
 AC 001382; Q9VAH1;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase precursor (EC 3.4.22.-) (dRICE).
 DE ICE OR CG7788.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 CX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 EC MEDLINE=97327558; PubMed=9184225;
 RA Fraser A.G., Evan G.I.;
 RT "Identification of a Drosophila melanogaster ICE/CED-3-related
 RT protease, dRICE.";
 RL EMBO J. 16:2805-2813 (1997).

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
 DE (ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity 2)
 DE (SCA-2).
 GN CASP7 OR MCH3.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=SYRIAN; TISSUE=Liver;
 RA MEDLINE=96224303; PubMed=8643593;
 RX Pai J.-T., Brown M.S., Goldstein J.L.;
 RT "Purification and cDNA cloning of a second apoptosis-related cysteine
 RT protease that cleaves and activates sterol regulatory element binding
 RT proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
 CC -!- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. Cleaves and activates sterol
 CC regulatory element binding proteins (SREBPs). Proteolytically
 CC cleaves poly(ADP-ribose) polymerase (PARP) at a 216-Asp-Gly-217
 CC bond. Overexpression promotes programmed cell death (By
 CC similarity).
 CC -!- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit
 CC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
 CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
 CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -!- SIMILARITY: Belongs to peptidase family C14.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC
 CC -----
 DR EMBL; U47332; AAC52595.1; -;
 DR HSSP; P42574; 1PAU.
 DR MEROPS; C14.004; -;
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR Pfam; PR00656; Peptidase_C14.
 DR PRINTS; PR00376; IL1BCENZME.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS0207; CASPASE_P10; 1.
 DR PROSITE; PS0208; CASPASE_P20; 1.
 KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 23
 FT CHAIN 24 198 CASPASE-7 SUBUNIT P20.
 FT PROPEP 199 206 BY SIMILARITY.
 FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
 FT ACT_SITE 144 144 BY SIMILARITY.
 FT ACT_SITE 186 186 BY SIMILARITY.
 SQ SEQUENCE 303 AA; 34037 MW; EA29356D90984648 CRC64;
 Query Match 2.4%; Score 10; DB 1; Length 303;
 Best Local Similarity 100.0%; Pred. No. 0.042;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 278 KPFLFFIQAC 287
 |||||||

Db 177 KPFLFFIQAC 186
 RESULT 7
 ICE7_MOUSE
 ID ICE7_MOUSE STANDARD; PRT; 303 AA.
 AC P97864; O08669;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine protease) (Apoptotic
 DE protease Mch-3).
 GN CASP7 OR MCH3 OR LICE2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA MEDLINE=97224489; PubMed=9070923;
 RX Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Fletcher F.A.;
 RT "Identification and mapping of Casp7, a cysteine protease resembling
 RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
 RL Genomics 40:86-93(1997).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=97236307; PubMed=9125129;
 RA Mukasa T., Khoroqui Y., Tsukahara T., Momoi M.Y., Kimura I.,
 RA Momoi T.;
 RT "Wortmannin enhances CPP32-like activity during neuronal
 RT differentiation of P19 embryonal carcinoma cells induced by retinoic
 RT acid.";
 RL Biochem. Biophys. Res. Commun. 232:192-197(1997).
 CC [3]
 CC SEQUENCE FROM N.A.
 CC STRAIN=C3H/An;
 RX MEDLINE=97190206; PubMed=9038361;
 RA van de Craen M., Vandenaabeele P., Declercq W., van den Brande I.,
 RA van Loo G., Molemans F., Schotte P., van Crielinge W., Beyaert R.,
 RA Fiers W.;
 RT "Characterization of seven murine caspase family members.";
 RL FEBS Lett. 403:61-69(1997).
 CC [4]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussidi T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. Cleaves and activates sterol
 CC regulatory element binding proteins (SREBPs). Overexpression
 CC promotes programmed cell death (By similarity).
 CC -!- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

length and shorter isoforms have been shown either to induce apoptosis or to reduce TNFRSF-triggered apoptosis. Lacks enzymatic (caspase) activity (By similarity).

-I- SUBUNIT: TNFRSF6 stimulation triggers recruitment to the death-inducing signalling complex (DISC) formed by TNFRSF6, FADD and caspase-8. A proteolytic fragment (p43) stays associated with the DISC (By similarity).

-I- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=1; Synonyms=FLIP-L, CASH alpha;

Isoid=035732-1; Sequence=Displayed;

Name=2; Synonyms=FLIP-S, CASH beta;

Isoid=035732-2; Sequence=VSP_000842, VSP_000843;

-I- TISSUE SPECIFICITY: Highly expressed in heart.

-I- DEVELOPMENTAL STAGE: At embryonic days E9.5 and E10.5 highest expression in developing heart.

-I- INDUCTION: Isoform 1 but not isoform 2 is activated by BCR cross-linking in primary B-cells. lacks the active sites residues involved in catalysis.

-I- PTM: Proteolytically processed; probably by caspase-8. Processing likely occurs at the DISC, generates subunit p43 and p12 (By similarity).

-I- SIMILARITY: Belongs to peptidase family C14.

-I- SIMILARITY: Contains 2 death effector (DED) domains.

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EMBL; Y14041; CAA74368.1; -

DR EMBL; Y14042; CAA74369.1; -

DR EMBL; U97076; AAC53281.1; -

DR HSP; Q15806; IQDU.

DR MEROPS; C14.974; -

DR MGD; MGI:1336166; Cflar.

DR InterPro; IPR001875; DED.

DR InterPro; IPR001309; ICE p20.

DR InterPro; IPR002398; Peptidase_C14.

DR Pfam; PF01335; DED; 2.

DR Pfam; PF00656; Peptidase_C14; 1.

DR SMART; SM00115; CASC; 1.

DR SMART; SM00031; DED; 2.

DR PROSITE; PS50208; CASPASE_P20; 1.

DR PROSITE; PS50168; DED; 2.

KW Apoptosis; Repeat; Alternative splicing.

FT CHAIN 1 380

FT CASP8 AND FADD-LIKE APOPTOSIS REGULATOR

FT SUBUNIT P43 (BY SIMILARITY).

FT CASP8 AND FADD-LIKE APOPTOSIS REGULATOR

FT SUBUNIT P12 (BY SIMILARITY).

FT DED 1.

FT DED 2.

FT CASPASE.

FT POLY-SER.

FT LQNGRSKEPRF -> VSLPVPYGVPA (in isoform 2).

FT /FTId=VSP_000842.

FT Missing (in isoform 2).

FT /FTId=VSP_000843.

FT MISSING (IN REF. 2).

FT SEQUENCE 484 AA; 55245 MW; 0BF7A92CB09F5F1F CRC64;

FT VARSPLIC 208 218

FT VARSPLIC 219 480

FT VARSPLIC 123 125

FT CONFLICT 123 125

FT SEQUENCE 484 AA; 55245 MW; 0; Indels 0; Gaps 0;

SQ

Query Match 2.2%; Score 9; DB 1; Length 484;

Best Local Similarity 100.0%; Pred. No. 0.67;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFIQ 285

DB 355 GKPKLFFIQ 363

RESULT 10

BRIL_ARATH STANDARD; PRT; 1196 AA.

ID BRIL_ARATH

AC O22476;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE BRASSINOSTEROID INSENSITIVE 1 precursor (EC 2.7.1.37) (AtBRIL1)

DE (Brassinosteroid LRR receptor kinase).

DE BRIL OR AT4G39400 OR F23K16.30.

GN Arabidopsis thaliana (Mouse-ear cress).

OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OC NCBI_TaxID=3702;

FN [1]

SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND MUTANTS BRIL-101;

RP BRIL-104; BRIL-113 AND BRIL-115.

RC STRAIN=cv. Columbia;

RA MEDLINE=97442355; PubMed=9298904;

EX Li J., Chory J.,

RT "A putative leucine-rich repeat receptor kinase involved in

RL brassinosteroid signal transduction.";

RL Cell 90:929-938 (1997).

FN [2]

SEQUENCE FROM N.A., FUNCTION, AND MUTANTS BRIL-5/DWF2-W41;

RP BRIL-6/BRIL-119/DWF2-399; BRIL-7/DWF2-WM3-2; BRIL-8/DWF2-WM6-2 AND

RP BRIL-9/DWF2-WB19.

RC STRAIN=cv. Wassilewskija-2, and cv. En-2;

RA MEDLINE=20027415; PubMed=10557222;

EX Noguchi T., Fujioaka S., Choe S., Takatsuto S., Yoshida S., Yuan H.,

RA Feldmann K.A., Tax F.E.,

RT "Brassinosteroid-insensitive dwarf mutants of Arabidopsis accumulate

RL brassinosteroids.";

RL Plant Physiol. 121:743-752 (1999).

FN [3]

SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE

RP SPECIFICITY, AND MUTANTS BRIL-1; BRIL-108; BRIL-117 AND BRIL-102.

RC STRAIN=cv. Columbia;

RA MEDLINE=20398322; PubMed=10938344;

EX Friedrichsen D.M., Joazeiro C.A.P., Li J., Hunter T., Chory J.,

RA "BRASSINOSTEROID-INSENSITIVE-1 is a ubiquitously expressed leucine-

RL rich repeat receptor serine/threonine kinase.";

RL Plant Physiol. 123:1247-1256 (2000).

FN [4]

SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RX MEDLINE=20083488; PubMed=10617198;

RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,

RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,

RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,

RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,

RA Kreis M., Delsen Y.M., Puigdomenech P., Watson M., Schmidheini T.,

RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,

RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Kidley F.,

RA Langham S.-A., McCullagh B., Bilham L., Robben J.,

RA Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,

RA Braeken M., Wajtsens I., Voet M., Bastiaens I., Aert R., Defoor E.,

RA Weitzenegger I., Bothe G., Ramsperger U., Hilbert H., Braun M.,

RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,

RA Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,

RA Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,

RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,

RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,

RA Clark L., Doggett J., Hall S., Kay M., Lennard N., Mayes R.,

RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,

RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,

RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Partmann B., Granderath K., Dauner D., Herzl A.,

RA Neumann S., Argiriou A., Vitale D., Liquori R., Piravandi E.,

RA Massenet O., Quigley F., Clabaud G., Muendlein A., Felber R.,

RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Chedford F., Cooke R., Berger C., Monfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
 RA Perez-Perez A., Farnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bialke C.,
 RA Frishman D., Haase D., Lemcke K., Meves H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threiden J.,
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Mix P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
 RA Chen E., Marra M.A., Martienssen R., McCombie W.R.,
 RA "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 RA thaliana".
 RT Nature 402:769-777(1999).
 RN [5]
 RN PHOSPHORYLATION.
 RP MEDLINE=20484044; PubMed=11027724;
 RX Oh M.-H., Ray W.K., Huber S.C., Asara J.M., Gage D.A., Clouse S.D.;
 RA "Recombinant BRASSINOSTEROID INSENSITIVE 1 receptor-like kinase
 RT autophosphorylates on serine and threonine residues and
 RT phosphorylates a conserved peptide motif in vitro";
 RL Plant Physiol. 124:751-766(2000).
 RN [6]
 RN STEROID BINDING.
 RP MEDLINE=20336852; PubMed=10875920;
 RX He Z., Wang Z.-Y., Li J., Zhu Q., Lamb C., Ronald P., Chory J.;
 RA "Perception of brassinosteroids by the extracellular domain of the
 RT receptor kinase BRI1";
 RL Science 288:2360-2363(2000).
 RN [7]
 RN SUBCELLULAR LOCATION, STEROID BINDING, AND AUTOPHOSPHORYLATION.
 RP MEDLINE=21168182; PubMed=11268216;
 RX Wang Z.-Y., Seto H., Fujioaka S., Yoshida S., Chory J.;
 RA "BRI1 is a critical component of a plasma-membrane receptor for plant
 RT steroids";
 RL Nature 410:380-383(2001).
 RN [8]
 RN SUBCELLULAR LOCATION, PHOSPHORYLATION, AND INTERACTION WITH BAK1.
 RP MEDLINE=22145926; PubMed=12150928;
 RX Nam K.H., Li J.;
 RA "BRI1/BAK1, a receptor kinase pair mediating brassinosteroid
 RT signaling";
 RL Cell 110:203-212(2002).
 RN [9]
 RN PHOSPHORYLATION, AND INTERACTION WITH BAK1.
 RP MEDLINE=22145927; PubMed=12150929;
 RX Li J., Wen J., Lease K.A., Duke J.T., Tax F.E., Walker J.C.;
 RA "BAK1, an Arabidopsis LRR receptor-like protein kinase, interacts with
 RT BRI1 and modulates brassinosteroid signaling";
 RL Cell 110:213-222(2002).
 CC -!- FUNCTION: Receptor with a serine/threonine-protein kinase
 CC activity. Regulates, in response to brassinosteroid binding, a
 CC signaling cascade involved in plant development, including
 CC expression of light- and stress-regulated genes, promotion of cell
 CC elongation, normal leaf and chloroplast senescence, and flowering.
 CC Binds brassinolide, and less effectively castasterone, but not
 CC 2,3,22,23-O-tetramethylbrassinolide or ecdysterone. May be involved
 CC in a feedback regulation of brassinosteroid biosynthesis.
 CC Phosphorylates BRI1-associated receptor kinase 1 (BAK1).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- ENZYME REGULATION: Activated by Ser and Thr phosphorylation.
 CC -!- SUBUNIT: Heterodimer with BAK1.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein; plasma membrane.
 CC -!- TISSUE SPECIFICITY: Expressed ubiquitously.

CC -!- DEVELOPMENTAL STAGE: Expressed constitutively in either dark- or
 CC light-grown seedlings.
 CC -!- DOMAIN: Contains one leucine-zipper motif and two pairs of
 CC conservatively spaced Cys (Cys pair 1 and 2) involved in forming
 CC heterodimers.
 CC -!- PTM: Phosphorylated on at least 12 sites, with a preference for
 CC Ser residues.
 CC -!- MISCELLANEOUS: A 70 amino acid island between the 20th and the
 CC 21th LRR is essential for the binding of brassinosteroids.
 CC -!- MISCELLANEOUS: Binding of brassinosteroid induces intramolecular
 CC autophosphorylation of BRI1. Interaction with BAK1 activates both
 CC receptor kinases and the full activation of either receptor kinase
 CC requires transphosphorylation by their partners. Optimum in vitro
 CC phosphorylation of the substrate requires Arg or Lys residues at
 CC P-3, P-4, and P-5 (relative to the phosphorylated amino acid at
 CC P-0).
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
 CC -!- SIMILARITY: Contains 25 leucine-rich (LRR) repeats.
 CC -----
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 CC -----
 CC EMBL; AF017056; AAC49810.1; -
 CC EMBL; AL078620; CAB44675.1; -
 CC EMBL; AL161595; CAB80603.1; -
 CC PIR; T09356; T09356.
 CC InterPro; IPR001611; LRR.
 CC InterPro; IPR007090; LRR_plant.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR008271; Ser_thr_pkin_AS.
 CC InterPro; IPR001245; Tyr_pkinase.
 CC Pfam; PF00560; LRR; 17.
 CC Pfam; PF00069; pkinase; 1.
 CC PRINTS; PR00019; LEURICHRPT.
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
 CC Transfaser; Kinase; Serine/threonine-protein kinase; Receptor;
 CC Steroid-binding; ATP-binding; Repeat; Signal; Transmembrane;
 CC Leucine-rich repeat; Glycoprotein; Phosphorylation.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 1196 BRASSINOSTEROID INSENSITIVE 1.
 FT TRANSMEM 793 813 POTENTIAL.
 FT REPEAT 98 121 LRR 1.
 FT REPEAT 122 146 LRR 2.
 FT REPEAT 148 169 LRR 3.
 FT REPEAT 172 197 LRR 4.
 FT REPEAT 199 221 LRR 5.
 FT REPEAT 222 244 LRR 6.
 FT REPEAT 245 268 LRR 7.
 FT REPEAT 269 290 LRR 8.
 Query Match 2.2%; Score 9; DB 1; Length 1196;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 131 IGSGGFGDV 139
 Db 889 IGSGGFGDV 897
 RESULT 11
 YK10 ARCFU
 ID YK10 ARCFU STANDARD; PRT; 232 AA.
 AC O28269;
 DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein AF2010.
 GN AF2010.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kerlavage A.R., Graham D.B., Kyrpides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Geckay J.D., Weidman J.F., McDonald L., Uterback T.,
 RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 CC -----
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 CC -----
 CC EMBL; Z99494; CAB16668.1; --
 CC EMBL; AL583924; CAC31098.1; --
 CC PIR; T45344; T45344.
 CC Leproma; ML2143; --
 CC Hypothetical protein; Transmembrane; Complete proteome.
 KW TRANSMEM 148 168 POTENTIAL.
 FT TRANSMEM 175 195 POTENTIAL.
 FT TRANSMEM 206 226 POTENTIAL.
 FT TRANSMEM 228 248 POTENTIAL.
 FT TRANSMEM 279 299 POTENTIAL.
 FT TRANSMEM 303 323 POTENTIAL.
 FT TRANSMEM 378 398 POTENTIAL.
 FT TRANSMEM 407 427 POTENTIAL.
 FT TRANSMEM 448 468 POTENTIAL.
 FT TRANSMEM 504 524 POTENTIAL.
 FT TRANSMEM 526 546 POTENTIAL.
 SQ SEQUENCE 579 AA; B6797F5FA0B22799 CRC64;
 CC -----
 CC Query Match 1.9%; Score 8; DB 1; Length 579;
 CC Best Local Similarity 100.0%; Pred. No. 8.3;
 CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 176 GLRTRTGS 183
 DB 17 GLRTRTGS 24
 CC -----
 CC RESULT 13
 CC BRIL LYCES STANDARD; PRT; 1207 AA.
 ID BRIL LYCES STANDARD; PRT; 1207 AA.
 AC Q8GUQ5;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Brassinosteroid LRR receptor kinase precursor (BC 2.7.1.37) (tBR11)
 DE (Altered brassinolide sensitivity 1) (Systemin receptor SR160).
 GN CURL3.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTANT CU3-ABS/ABS1.
 RX MEDLINE=22356999; PubMed=12468734;
 RA Montoya T., Nomura T., Farrar K., Kaneta T., Yokota T., Bishop G.J.;
 RT "Cloning the tomato curl3 gene highlights the putative dual role of
 RT the leucine-rich repeat receptor kinase tBR11/SR160 in plant steroid
 RT hormone and peptide hormone signaling.";
 RL Plant Cell 14:3163-3176(2002).
 RN [2]
 RP SUBSTRATE BINDING.
 RX MEDLINE=22103620; PubMed=12060717;
 RA Scheer J.M., Ryan C.A. Jr.;
 RT "The systemin receptor SR160 from Lycopersicon peruvianum is a member
 RT of the LRR receptor kinase family.";
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein AF2010.
 GN AF2010.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kerlavage A.R., Graham D.B., Kyrpides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Geckay J.D., Weidman J.F., McDonald L., Uterback T.,
 RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 CC -----
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 CC -----
 CC EMBL; AE000964; AAB89255.1; --
 CC PIR; A69501; A69501.
 CC TIGR; AF2010; --
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 10 32 POTENTIAL.
 SQ SEQUENCE 232 AA; 26339 MW; 7B94ABE576DB1476 CRC64;
 CC -----
 CC Query Match 1.9%; Score 8; DB 1; Length 232;
 CC Best Local Similarity 100.0%; Pred. No. 3.7;
 CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 174 ESGLRTRT 181
 DB 29 ESGLRTRT 36
 CC -----
 CC RESULT 12
 CC Y876 MYCLE STANDARD; PRT; 579 AA.
 ID Y876 MYCLE STANDARD; PRT; 579 AA.
 AC Q33057;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein ML2143.
 GN ML2143 OR MLCB57.28C.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Eigmeier K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

21th LRR is essential for the binding of brassinosteroids (By similarity).

-!- MISCELLANEOUS: SR160 is almost identical to BR11, a brassinosteroid receptor identified in *Lycopersicon esculentum*. Competition experiments indicate that brassinosteroid and systemin are probably perceived by different regions of the receptor.

CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. Contains 24 leucine-rich (LRR) repeats.

CC -!- SIMILARITY: Contains 24 leucine-rich (LRR) repeats.

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CC -----

EMBL: AY112661; ANM48285.1; --

DR InterPro; IPR001611; LRR.

DR InterPro; IPR007090; LRR_plant.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR008271; Ser_thr_pkin_AS.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR InterPro; IPR001245; Tyr_pkinase.

DR Pfam; PF00560; LRR; 19.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00019; LEURICHRPT.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00220; S_TKc; 1.

DR SMART; SM00219; TyrKc; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW Plant defense; Transferase; Kinase; Serine/threonine-protein kinase;

KW Receptor; ATP-binding; Steroid-binding; Repeat; Signal; Transmembrane;

KW Leucine-rich repeat; Glycoprotein.

FT SIGNAL 1 34

FT CHAIN 35 1207 SYSTEMIN RECEPTOR SR160.

FT TRANSMEM 803 823 POTENTIAL.

FT REPEAT 80 106 LRR 1.

FT REPEAT 107 131 LRR 2.

FT REPEAT 133 158 LRR 3.

FT REPEAT 159 182 LRR 4.

FT REPEAT 184 206 LRR 5.

FT REPEAT 211 235 LRR 6.

FT REPEAT 237 255 LRR 7.

FT REPEAT 256 280 LRR 8.

FT REPEAT 282 307 LRR 9.

FT REPEAT 327 350 LRR 10.

FT REPEAT 351 375 LRR 11.

FT REPEAT 376 399 LRR 12.

FT REPEAT 400 424 LRR 13.

FT REPEAT 426 450 LRR 14.

FT REPEAT 452 474 LRR 15.

FT REPEAT 475 498 LRR 16.

FT REPEAT 499 522 LRR 17.

FT REPEAT 524 546 LRR 18.

FT REPEAT 547 570 LRR 19.

FT REPEAT 572 594 LRR 20.

FT REPEAT 596 619 LRR 21.

FT REPEAT 622 645 LRR 22.

FT REPEAT 647 670 LRR 23.

FT REPEAT 671 694 LRR 24.

FT REPEAT 695 718 LRR 25.

FT REPEAT 719 742 LRR 26.

FT REPEAT 743 766 LRR 27.

FT REPEAT 767 790 LRR 28.

FT REPEAT 791 814 LRR 29.

FT REPEAT 815 838 LRR 30.

FT DOMAIN 888 902 ATP (BY SIMILARITY).

FT NP_BIND 894 902 ATP (BY SIMILARITY).

FT BINDING 916 916 ATP (BY SIMILARITY).

FT ACT_SITE 1014 1014 CYS PAIR 1.

FT SITE 71 78 CYS PAIR 2.

FT SITE 771 779 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	235	235	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	245	245	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	287	287	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	339	339	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	363	363	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	412	412	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	449	449	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	521	521	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	556	556	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	584	584	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	646	646	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	662	662	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	724	724	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	746	746	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	767	767	N-LINKED (GLCNAC. . .)	(POTENTIAL).
SQ	SEQUENCE	1207 AA;	131963 MW;	1422D1DFDA458073 CRC64;	

Query Match 1.9%; Score 8; DB 1; Length 1207;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	132	GSGGFGDV	139
Db	895	GSGGFGDV	902

RESULT 15

RPOC_CHLPN STANDARD; PRT; 1393 AA.

AC Q9Z999; Q9JSJ7; Q9K211;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase beta' chain) (RNA polymerase beta' subunit).
DE RPOC OR CPN0082 OR CP0693 OR CPB0082.
GN Chlamydia pneumoniae (Chlamydophila pneumoniae).
OS Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OC NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206066; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA";
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=TW-183;
RA Geng M., Schuhmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
Schneider S., Pohl T., Essig A., Marre R., Melchers K.;

"The genome sequence of Chlamydia pneumoniae TW183 and comparison with other Chlamydia strains based on whole genome sequence analysis.";
 Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates.
 -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + (RNA) (N).
 -!- SUBUNIT: The enzyme consists of the sigma chain and the core enzyme which is composed of 2 alpha chains, 1 beta chain, and 1 beta chain.
 -!- SIMILARITY: Belongs to the RNA polymerase beta' chain family.
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 EMBL; AE001593; AAD18035.1; -
 EMBL; AE002228; AAF38501.1; ALT_INIT.
 EMBL; AP002545; BAA98292.1; -
 EMBL; AE017157; AAP98015.1; -
 DR PIR; B86501; B86501.
 DR PIR; E72122; E72122.
 DR HSP; O9KWU6; 1HQM.
 DR TIGR; CP0693; -
 DR InterPro; IPR000722; RNA_pol_A.
 DR InterPro; IPR007080; RNA_pol_Rpb1_1.
 DR InterPro; IPR007066; RNA_pol_Rpb1_3.
 DR InterPro; IPR007083; RNA_pol_Rpb1_4.
 DR InterPro; IPR007081; RNA_pol_Rpb1_5.
 DR InterPro; IPR006592; RNA_pol_N.
 DR Pfam; PF04997; RNA_pol_Rpb1_1; 1.
 DR Pfam; PF00623; RNA_pol_Rpb1_2; 1.
 DR Pfam; PF04983; RNA_pol_Rpb1_3; 1.
 DR Pfam; PF05000; RNA_pol_Rpb1_4; 1.
 DR Pfam; PF04998; RNA_pol_Rpb1_5; 1.
 DR SMART; SM00663; RPOLA_N; 1.
 KW Transferrase; DNA-directed RNA polymerase; Transcription;
 KW Complete proteome.
 FT CONFLICT 1031 1031 A -> G (IN REF. 1).
 SQ SEQUENCE 1393 AA; 154900 MW; E0734FF236C6FDE8 CRC64;
 Query Match 1.9%; Score 8; DB 1; Length 1393;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 377 SEDLQSL 384
 Db 194 SEDLQSL 201
 RESULT 16
 GCSE MYCLE STANDARD; PRT; 132 AA.
 AC Q32920;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Glycine cleavage system H protein.
 DE GCYH OR ML2077 OR MLCB1788.37C.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,

Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin M., Holroyd S., Hornsby T., Jagsels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajadream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.;
 "Massive gene decay in the leprosy bacillus.";
 Nature 409:1007-1011(2001).
 -!- FUNCTION: The glycine cleavage system catalyzes the degradation of glycine. The H protein shuttles the methylamine group of glycine from the P protein to the T protein (By similarity).
 -!- COFACTOR: The H chain contains a covalently-bound lipoyl cofactor (By similarity).
 -!- SUBUNIT: The glycine cleavage system is composed of four proteins: P, T, L and H (By similarity).
 -!- SIMILARITY: Belongs to the gcvh family.
 -!- SIMILARITY: Contains 1 lipoyl-binding domain.
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 EMBL; AL008609; CAA15469.1; -
 EMBL; AL583924; CAC31032.1; -
 DR PIR; T44759; T44759.
 DR HSP; P16048; 1HTP.
 DR Leproma; ML2077; -
 DR HAMAP; MF 00272; -; 1.
 DR InterPro; IPR002930; GCV_H.
 DR InterPro; IPR003016; Lipoyl_BS.
 DR Pfam; PF01597; GCV_H; 1.
 DR TIGRFAMS; TIGR00527; gcvh; 1.
 DR PROSITE; PS00189; LIPOYL; 1.
 KW Lipoyl; Complete proteome.
 FT BINDING 65 65 LIPOYL (BY SIMILARITY).
 SQ SEQUENCE 132 AA; 14070 MW; 2DBF05D69BA1C6AA CRC64;
 Query Match 1.7%; Score 7; DB 1; Length 132;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 138 DVGAL 144
 Db 109 DVGAL 115
 RESULT 17
 PTH CHLPN STANDARD; PRT; 180 AA.
 AC Q9Z6V6; Q9JQC0;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Peptidyl-tRNA hydrolase (EC 3.1.1.29) (PTH).
 GN PTH OR CPN0950 OR CP0909 OR CP0987.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CWL029;
 RX MEDLINE=99206606; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
 RL Nat. Genet. 21:385-389(1999).
 RN [2]

DE protein B).
 GN GIDB OR ML14481.
 OS Rhizobium loti (Mesorhizobium loti).
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Phyllobacteriaceae; Mesorhizobium.
 OK NCBI_TaxID=381;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shampo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 CC -!- FUNCTION: Probable S-adenosyl-L-methionine dependent
 CC methyltransferase specific for a sterol and/or lipid substrate (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the gidB family.
 CC
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 CC
 CC EMBL; AP003004; BAB51128.1; -.
 DR HAMAP; MF 00074; -; 1.
 DR InterPro; IPR003682; GidB.
 DR Pfam; PF02527; GidB; 1.
 DR ProDom; PD004441; GidB; 1.
 DR TIGRFAMS; TIGR00138; gidB; 1.
 DR Transferase; Methyltransferase; Complete proteome.
 KW SEQUENCE 210 AA; 23107 MW; F798AB0C33329AB CRC64;
 SQ
 Query Match 1.7%; Score 7; DB 1; Length 210;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 129 VDIGSGG 135
 Db 71 VDIGSGG 77
 RESULT 20
 RS3_RALSO STANDARD; PRT; 264 AA.
 AC Q8XV18;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 30S ribosomal protein S3
 GN RSCC OR RSC3013 OR RSC1076.
 OS Ralstonia solanacearum (pseudomonas solanacearum).
 CC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 CC Burkholderiaceae; Ralstonia.
 OK NCBI_TaxID=305;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brottier P., Camus J.C., Catolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
 RA Siguer P., Tiebaut P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";

RL Nature 415:497-502(2002).
 CC -!- FUNCTION: Binds the lower part of the 30S subunit head. Binds mRNA
 CC in the 70S ribosome, positioning it for translation (By
 CC similarity).
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight complex
 CC with proteins S10 and S14 (By similarity).
 CC -!- SIMILARITY: Belongs to the S3P family of ribosomal proteins.
 CC -!- SIMILARITY: Contains 1 KH type-2 domain.
 CC
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 CC
 CC EMBL; AL646073; CAD16722.1; -.
 DR HAMAP; MF 01309; -; 1.
 DR InterPro; IPR004087; KH dom.
 DR InterPro; IPR009019; KH prok.
 DR InterPro; IPR004044; KH TYPE 2.
 DR InterPro; IPR001351; Ribosomal_S3_C.
 DR InterPro; IPR008282; Ribosomal_S3_N.
 DR InterPro; IPR005704; S3_bact.
 DR Pfam; PF00013; KH; 1.
 DR Pfam; PF00189; Ribosomal_S3_C; 1.
 DR Pfam; PF00417; Ribosomal_S3_N; 1.
 DR SMART; SM00322; KH; 1.
 DR TIGRFAMS; TIGR01009; rpsc_bact; 1.
 DR PROSITE; PS00823; KH TYPE 2; 1.
 DR PROSITE; PS00548; RIBOSOMAL_S3; 1.
 KW Ribosomal protein; RNA-binding; rRNA-binding; Complete proteome.
 FT DOMAIN 39 107 KH TYPE-2.
 SQ SEQUENCE 264 AA; 29738 MW; 72BBCACF1EC2DD3E CRC64;
 Query Match 1.7%; Score 7; DB 1; Length 264;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 114 EIRKPEV 120
 Db 105 EIRKPEV 111
 RESULT 21
 NHS_STRAS
 ID NHS_STRAS STANDARD; PRT; 274 AA.
 AC P52391;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE 23S rRNA methyltransferase (EC 2.1.1.-) (23S rRNA methylase).
 GN NHS.
 OS Streptomyces actuosus.
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Streptomycineae; Streptomycetaceae; Streptomyces.
 OK NCBI_TaxID=1885;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 25421;
 RX MEDLINE=90382703; PubMed=2401410;
 RA Li Y., Dosch D.C., Strohl W.R., Floss H.G.;
 RT "Nucleotide sequence and transcriptional analysis of the nosiheptide-
 RT resistance gene from Streptomyces actuosus.";
 RL Gene 91:9-17(1990).
 CC -!- FUNCTION: CONFERS RESISTANCE TO ANTIBIOTIC NOSIHEPTIDE.
 CC -!- SIMILARITY: TO S.AZUREUS TSR.
 CC
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CC -----

DR EMBL; U75434; AAB17875.1; -;
DR PIR; JQ0686; JQ0686.
DR InterPro; IPR001537; SpoU_methylase.
DR InterPro; IPR006795; TSNR_N.
DR Pfam; PF00588; SpoU_methylase; 1.
DR Pfam; PF04705; TSNR_N; 1.
DR ProDom; PD001243; SpoU_methylase; 1.
DR Antibiotic resistance; Transferase; Methyltransferase.
KW
SQ SEQUENCE 274 AA; 291.83 MW; 9FA2CL1B2E8BF24D CRC64;

Query Match 1.7%; Score 7; DB 1; Length 274;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ADRELLR 10
DB 156 ADRELLR 162

RESULT 22
SDSB_PSES9 STANDARD; PRT; 306 AA.
AC P52686;

DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE SDS degradation transcriptional activation protein.

GN SDSB.

OS Pseudomonas sp. (strain ATCC 19151).

OC Bacteria; Proteobacteria.

OX NCBI_TaxID=315;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92267380; PubMed=1587481;

RA Davison J., Brunel F., Phanopoulos A., Prozzi D., Terpstra P.;

RT "Cloning and sequencing of Pseudomonas genes determining sodium

RT dodecyl sulfate biodegradation.";

RL Gene 114:19-24(1992).

CC -!- FUNCTION: ACTIVATES THE TRANSCRIPTION OF THE SDSA GENE FOR

CC -!- SODIUM DODECYL SULFATE (SDS) DEGRADATION.

CC -!- SIMILARITY: Contains 1 HTH lyser-type DNA-binding domain.

CC -----
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CC -----

DR EMBL; M86744; AAA25988.1; -;
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PROSITE; PS00931; HTH_LYSR; 1.
KW Transcription regulation; DNA-binding; Activator.
FT DOMAIN 1 59 HTH_LYSR-TYPE.
FT DNA_BIND 19 38 H-T-H MOTIF (POTENTIAL).
SQ SEQUENCE 306 AA; 329.55 MW; BE1A6EACF3FE24FA CRC64;

Query Match 1.7%; Score 7; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 LALLELA 220
DB 256 LALLELA 262

RESULT 23

G3P_THEVO STANDARD; PRT; 338 AA.

AC Q97B08;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.59) (GAPDH)
DE (NAD(P)-dependent glyceraldehyde-3-phosphate dehydrogenase).
DE GAP OR TV0457 OR TVG0444310.

OS Thermoplasma volcanium.

OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;

OC Thermoplasmataceae; Thermoplasma.

OX NCBI_TaxID=50339;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=GSS1 / DSM 4299 / JCM 9571;

RX MEDLINE=20570466; PubMed=11121031;

RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,

RA Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,

RA Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;

RT "Archaeal adaptation to higher temperatures revealed by genomic

RT sequence of Thermoplasma volcanium".

RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).

CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +

CC NAD(P)(+) = 3-phospho-D-glyceroyl phosphate + NAD(P)H.

CC -!- PATHWAY: Second phase of glycolysis; first step.

CC -!- SUBUNIT: Homotetramer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate

CC dehydrogenase family.
CC -----

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CC -----

DR EMBL; AP000992; BAB59599.1; -;

DR HAMAP; MF_00559; -; 1.

DR InterPro; IPR000173; GAP_dhdhydrogenase.

DR InterPro; IPR006436; GAPDH-II_archae.

DR Pfam; PF00044; gpdh; 1.

DR Pfam; PF02800; gpdh_C; 1.

DR ProDom; PD007761; GAPDH-II_archae; 1.

DR TIGRFAMs; TIGR01546; GAPDH-II_archae; 1.

DR PROSITE; PS0071; GAPDH; 1.

DR PROSITE; PS0071; GAPDH; 1.

KW Glycolysis; Oxidoreductase; NAD; NADP; Complete proteome.

FT BINDING 139 139 GLYCERALDEHYDE 3-PHOSPHATE (BY

FT BINDING 139 139 SIMILARITY).

FT SEQUENCE 338 AA; 37374 MW; C9BD53DFD4722F34 CRC64;

QY SEQUENCE 338 AA; 37374 MW; C9BD53DFD4722F34 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 338;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 RVANAVS 392

DB 15 RVANAVS 21

RESULT 24

TRPD_AERPE

ID TRPD_AERPE STANDARD; PRT; 345 AA.

AC Q9Y872;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Anthranilate phosphoribosyltransferase (EC 2.4.2.18).

FT TRPD OR APE2551.

```

OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawaiyabashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
CC -!- CATALYTIC ACTIVITY: Anthranilate + phosphoribosyl-diphosphate =
CC N-5'-phosphoribosyl-anthranilate + diphosphate.
CC -!- PATHWAY: Tryptophan biosynthesis; second step.
CC -!- SIMILARITY: Belongs to the anthranilate phosphoribosyltransferase
CC family.
CC
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CC
CC EMBL; AP000064; BAA81568.1; -.
CC PIR; H72488; H72488.
CC HAMAP; MF 00211; -.
CC InterPro; IPR005940; Ant_phospho_trans.
CC InterPro; IPR000312; Glyco_trans_3.
CC Pfam; PF02885; Glycos_trans_3N; 1.
CC Pfam; PF00591; Glycos_transf_3; 1.
CC ProDom; PD001864; Glyco_transf_3; 1.
CC TIGRFAMs; TIGR01245; trpD; 1_3; 1.
CC TrpTophan biosynthesis; Transferase; Glycosyltransferase;
KW Complete proteome. 305
KW DOMAIN 299
KW FT ACT_SITE 299 305 POLY-ALA.
SQ SEQUENCE 345 AA; 36449 MW; 5CBF8E8B4EAC2B CRC64;

Query Match 1.7%; Score 7; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 LRVANAV 391
DB 270 LRVANAV 276
|||||
TRUD_SALTY
ID TRUD_SALTY STANDARD; PRT; 349 AA.
AC Q8Z473;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE tRNA pseudouridine synthase D (EC 4.2.1.70) (Pseudouridylylate synthase)
DE (Uracil hydrolyase).
GN TRUD OR STV3053 OR T2829.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,

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RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagsis K.,
RA Krogh A., Larsen T.S., Leach S., Moule S., O'Goara P., Parry C.,
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -!- FUNCTION: Responsible for synthesis of pseudouridine from
CC uracil-13 in transfer RNAs (By similarity).
CC -!- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine
CC + 5'-phosphate + H(2)O.
CC -!- SIMILARITY: Belongs to the pseudouridine synthase truD family.
CC
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CC
CC EMBL; AL627276; CAD06034.1; -.
CC EMBL; AE016843; AA070386.1; -.
CC HAMAP; MF_01082; -.
CC InterPro; IPR001656; UPF0024.
CC Pfam; PF01142; UPF0024; 1.
CC TIGRFAMs; TIGR00094; TIGR00094; 1.
CC PROSITE; PS01268; UPF0024; 1.
KW tRNA processing; Lyase; Complete proteome.
KW FT ACT_SITE 80 80 BY SIMILARITY.
SQ SEQUENCE 349 AA; 39361 MW; 548A1BA51A8F3E7A CRC64;

Query Match 1.7%; Score 7; DB 1; Length 349;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 LQSLILR 386
DB 285 LQSLILR 291
|||||
TRUD_SALTY
ID TRUD_SALTY STANDARD; PRT; 349 AA.
AC Q8ZMF8;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE tRNA pseudouridine synthase D (EC 4.2.1.70) (Pseudouridylylate synthase)
DE (Uracil hydrolyase).
GN TRUD OR STM2928.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

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RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Master genome sequence of *Salmonella enterica* serovar Typhimurium
 RT L12.",
 RL Nature 413:852-856(2001).
 CC -!- FUNCTION: Responsible for synthesis of pseudouridine from
 CC uracil-13 in transfer RNAs (By similarity).
 CC -!- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine
 CC 5'-phosphate + H(2)O.
 CC -!- SIMILARITY: Belongs to the pseudouridine synthase truD family.
 CC
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 CC
 CC EMBL; AE008833; AAL21808.1; -.
 CC STyGene; SG????; truD.
 CC HAMAP; MF_01082; -; 1.
 CC InterPro; IPR001656; UPF0024.
 CC Pfam; PF01142; UPF0024; 1..000094; 1.
 CC TIGRFAMs; TIGR00094; TIGR00094; 1.
 CC PROSITE; PS01268; UPF0024; 1.
 CC TRNA processing; Lyase; Complete proteome.
 CC ACT SITE 80 80 BY SIMILARITY.
 CC SEQUENCE 349 AA; 39332 MW; 5357437747CDSA51 CRC64;
 CC
 CC Query Match 1.7%; Score 7; DB 1; Length 349;
 CC Best Local Similarity 100.0%; Pred. No. 55;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 380 LQSLLLR 386
 CC Db 285 LQSLLLR 291
 CC
 CC RESULT 27
 CC ID RAL1 YEAST STANDARD; PRT; 401 AA.
 CC AC P48581;
 CC DT 01-FEB-1996 (Rel. 33, Created)
 CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
 CC DT 01-NOV-1997 (Rel. 35, Last annotation update)
 CC DE DNA damage checkpoint control protein RAD17.
 CC GN RAD17 OR YOR368W.
 CC OS Saccharomyces cerevisiae (Baker's yeast).
 CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CC OX NCBI_TaxID=4932;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=96211370; PubMed=8649984;
 CC RA Siede W., Dianova I., Nussbaumer G., Portillo V., Rodriguez R.,
 CC Nunes E., Friedberg E.C.;
 CC RT "Cloning and characterization of RAD17, a gene controlling cell cycle
 CC responses to DNA damage in *Saccharomyces cerevisiae*.";
 CC RL Nucleic Acids Res. 24:1669-1675(1996).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RA Lydall D., Weinert T.;
 CC RN Submitted (XXX-1995) to the EMBL/GenBank/DBJ databases.
 CC [3]
 CC RP SEQUENCE FROM N.A.
 CC RA Delius H., Hebling U., Hofmann B.;
 CC RN Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Putative exonuclease involved in DNA damage checkpoint
 CC control.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- SIMILARITY: SOME, TO S.POMBE RAD1 AND TO U.MAYDIS RECL.

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 CC
 CC EMBL; U37460; AAA80545.1; -.
 CC DR EMBL; U30796; AAA93250.1; -.
 CC DR EMBL; Z75276; CAA99699.1; -.
 CC DR PIR; S59670; S59670.
 CC Germonline; 143956; -.
 CC SGD; S0005895; RAD17.
 CC GO; GO:0005634; C:nucleus; IPI.
 CC GO; GO:0000077; P:DNA damage response, signal transduction re. .; IMP.
 CC GO; GO:0007131; P:meiotic recombination; IMP.
 CC DR InterPro; IPR003021; Rad1_Recl.
 CC DR Pfam; PF02144; Rad1; 1.
 CC DR PRINTS; PR01245; RAD1RECL.
 CC DR DNA damage; DNA repair; Hydrolase; Exonuclease; Nuclear protein.
 CC KW VARIANT 128 128 E -> K (IN RAD17-1; UV-SENSITIVE).
 CC SQ SEQUENCE 401 AA; 45579 MW; BFF7074676C483C9 CRC64;
 CC
 CC Query Match 1.7%; Score 7; DB 1; Length 401;
 CC Best Local Similarity 100.0%; Pred. No. 63;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 29 LLSRELF 35
 CC Db 61 LLSRELF 67
 CC
 CC RESULT 28
 CC ID YBR3 YEAST STANDARD; PRT; 404 AA.
 CC AC P38083;
 CC DT 01-OCT-1994 (Rel. 30, Created)
 CC DT 01-OCT-1994 (Rel. 30, Last sequence update)
 CC DT 01-NOV-1995 (Rel. 32, Last annotation update)
 CC DE Hypothetical 46.4 kDa protein in ORC2-TIP1 intergenic region.
 CC GN YBR063C OR YBR0610.
 CC OS Saccharomyces cerevisiae (Baker's yeast).
 CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CC OX NCBI_TaxID=4932;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=S288c;
 CC RA Domdey H., Gassenhuber H., Obermaier B., Piravandi E.;
 CC RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 CC
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 CC
 CC EMBL; Z35932; CAA85006.1; -.
 CC DR PIR; S45923; S45923.
 CC Germonline; 138606; -.
 CC SGD; S000267; YBR063C.
 CC KW Hypothetical protein; Transmembrane.
 CC FT TRANSMEM 35 55 POTENTIAL.
 CC FT TRANSMEM 92 112
 CC SQ SEQUENCE 404 AA; 46444 MW; B2CC066A6B0A0670 CRC64;
 CC
 CC Query Match 1.7%; Score 7; DB 1; Length 404;
 CC Best Local Similarity 100.0%; Pred. No. 63;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 307 SPGSNPE 313
DB 215 SPGSNPE 221
|||||
|||||

RESULT 29
BACA RHIME
ID BACA RHIME STANDARD; PRT; 420 AA.
AC Q08120;
DT 01-OCT-1994 (Rel. 30, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bacteroid development protein baca.
GN BACA OR RB1125 OR SMB20999
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Plasmid pSymb (megaplasmid 2).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=93339575; PubMed=8393417;
RA Glazebrook J., Ichige A., Walker G.C.;
RA "A Rhizobium meliloti homolog of the Escherichia coli peptide-
RT antibiotic transport protein SbmA is essential for bacteroid
RT development";
RL Genes Dev. 7:1485-1497 (1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396508; PubMed=11481431;
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA Vorhoefer F.J., Hernandez-Lucas I., Becker A., Gouzy J.,
RA Golding B., Puelher A.;
RA "The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).
CC -1- FUNCTION: FUNCTIONS IN THE TRANSPORT OF MOLECULES, POSSIBLY
CC PEPTIDES, ACROSS THE INNER MEMBRANE. IS ESSENTIAL FOR BACTEROID
CC DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -1- TISSUE SPECIFICITY: NODULES.
CC -1- SIMILARITY: STRONG. TO E.COLI SBMA.
CC
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CC
CC EMBL: X73522; CAA51918.1; -.
CC DR EMBL; AL603646; CAC49525.1; -.
CC DR F1R; A47649; A47649.
CC DR F1R; E95982; E95982.
KW Transport; Transmembrane; Inner membrane; Plasmid; Complete proteome.
FT TRANSMEM 11 31 POTENTIAL.
FT TRANSMEM 61 81 POTENTIAL.
FT TRANSMEM 92 112 POTENTIAL.
FT TRANSMEM 143 163 POTENTIAL.
FT TRANSMEM 210 230 POTENTIAL.
FT TRANSMEM 247 267 POTENTIAL.
FT TRANSMEM 336 356 POTENTIAL.
FT CONFLICT 128 128 A -> P (IN REF. 1).
SQ SEQUENCE 420 AA; 47848 MW; 548496A86AD1D0FE CRC64;

Query Match 1.7%; Score 7; DB 1; Length 420;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 31
RECA TROWT
ID RECA TROWT STANDARD; PRT; 437 AA.
AC Q83MS9; Q83NC5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)

QY 263 IVNIENG 269
DB 240 IVNIENG 246
|||||
|||||

Query Match 1.7%; Score 7; DB 1; Length 426;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFI 284
DB 8 KPCLFFI 14
|||||
|||||

RESULT 30
LIP7 CANAL
ID LIP7 CANAL STANDARD; PRT; 426 AA.
AC Q9P4E7;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lipase 7 precursor (EC 3.1.1.3).
GN LIP7.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.
RC STRAIN=SC5314;
RX MEDLINE=21014758; PubMed=11131027;
RA Hube B., Stehr E., Bossenz M., Mazur A., Kretschmar M., Schaefer W.;
RA "Secreted lipases of Candida albicans: cloning, characterisation and
RT expression analysis of a new gene family with at least ten members.";
RL Arch. Microbiol. 174:362-374 (2000).
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
CC family.
CC
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CC
CC EMBL: AF191320; AAF79928.1; -.
CC DR InterPro; IPR005152; LIP.
CC DR Pfam; PF03583; LIP; 1.
KW Lipid degradation; Hydrolase; Signal; Glycoprotein; Multigene family.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 426 LIPASE 7.
FT ACT_SITE 190 190 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 321 321 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 175 175 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 378 378 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 379 379 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 422 422 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 426 AA; 47854 MW; 2DBBABC4BCC6A85 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 426;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 IVNIENG 269
DB 240 IVNIENG 246
|||||
|||||

Query Match 1.7%; Score 7; DB 1; Length 420;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 32
IFR2 HUMAN

DR Pfam; PF04836; IPRD C; 1.
 SQ SEQUENCE 442 AA; 48047 MW; CB54F2118C0CBA7A CRC64;
 Query Match 1.7%; Score 7; DB 1; Length 442;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 140 GALESLR 146
 |||||
 Db 94 GALESLR 100
 RESULT 33
 ICE8 MOUSE
 ID ICE8 MOUSE STANDARD; PRT; 480 AA.
 AC O8910; O35669;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-8 precursor (EC 3.4.22.-).
 GN CASP8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=129/SVJ;
 RA Sakamaki K., Tsukumo S.-I., Yonehara S.;
 RT "Molecular cloning and characterization of mouse caspase-8";
 RL Eur. J. Biochem. 253:399-405(1998).
 [2]
 RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC MEDLINE=9316661; PubMed=9654089;
 RA van der Brande I., Mandruzzato S., van der Bruggen P., Fiers W.,
 RT "Molecular cloning and identification of murine caspase-8";
 RL J. Mol. Biol. 284:1017-1026(1998).
 [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon, and Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Carninci P., Frange C.,
 RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 RN SEQUENCE OF 57-476 FROM N.A.
 RP Kioschis P., Kischkel F., Poustka A., Kramer P.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Most upstream protease of the activation cascade of
 CC caspases responsible for the TNFRSF6/FAS mediated and TNFRSF1A
 CC induced cell death. Binding to the adapter molecule FADD recruits
 CC it to either receptor. The resulting aggregate called death-
 CC inducing signaling complex (DISC) performs CASP8 proteolytic

CC activation. The active dimeric enzyme is then liberated from the
 CC DISC and free to activate downstream apoptotic proteases.
 CC proteolytic fragments of the N-terminal propeptide (termed CAP3,
 CC CAP5 and CAP6) are likely retained in the DISC. Cleaves and
 CC activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
 CC participate in the G2M6 apoptotic pathways. Cleaves ADPRT.
 CC Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC.
 CC Likely target for the coxop virus CRMA death inhibitory protein.
 CC -!- ENZYME REGULATION: Inhibited by Z-VAD-FK, Crma and P35.
 CC -!- SUBUNIT: Heterodimer of a 18 kDa (P18) and a 10 kDa (P10) subunit.
 CC Interacts with Fadd, Cflar and Peals (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed in a wide variety of tissues.
 CC Highest expression in spleen, thymus, lung, liver and kidney.
 CC Lower expression in heart, brain, testis and skeletal muscle.
 CC -!- DEVELOPMENTAL STAGE: In the embryo, highest expression occurs at
 CC day 7.
 CC -!- PTM: Generation of the subunits requires association with the
 CC death-inducing signaling complex (DISC), whereas additional
 CC processing is likely due to the autocatalytic activity of the
 CC activated protease. G2MB and CASP10 can be involved in these
 CC processing events (By similarity).
 CC -!- SIMILARITY: Belongs to peptidase family C14.
 CC -!- SIMILARITY: Contains 2 death effector (DED) domains.
 CC
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 CC
 CC -----
 CC EMBL; AF067841; AAC40132.1; -
 CC EMBL; AF067835; AAC40132.1; JOINED.
 CC EMBL; AF067836; AAC40132.1; JOINED.
 CC EMBL; AF067837; AAC40132.1; JOINED.
 CC EMBL; AF067838; AAC40132.1; JOINED.
 CC EMBL; AF067839; AAC40132.1; JOINED.
 CC EMBL; AF067840; AAC40132.1; JOINED.
 CC EMBL; AF067834; AAC40131.1; -
 CC EMBL; AJ007749; CAA07877.1; -
 CC EMBL; BC006737; AAH06737.1; -
 CC EMBL; BC049955; AAH49955.1; -
 CC EMBL; AJ000641; CAA04196.1; -
 CC HSSP; QJ5806; IQDU.
 CC MEROPS; C14.009; -
 CC MGD; MGI:1261423; Casp8.
 CC GO; GO:0005737; C:cytoplasm; IDA.
 CC GO; GO:0005634; C:nucleus; IDA.
 CC GO; GO:004205; F:caspase-8 activity; IDA.
 CC GO; GO:0006915; P:apoptosis; IDA.
 CC InterPro; IPR001875; DED.
 CC InterPro; IPR021138; ICE_p10.
 CC InterPro; IPR001309; ICE_p20.
 CC InterPro; IPR002398; Peptidase_C14.
 CC Pfam; PF01335; DED; 2.
 CC Pfam; PF00656; Peptidase_C14; 1.
 CC PRINTS; PR00376; IL1BCENZYME.
 CC SMART; SM00115; CASC; 1.
 CC SMART; SM00031; DED; 2.
 CC PROSITE; PS01122; CASPASE_CYS; 1.
 CC PROSITE; PS01121; CASPASE_HIS; 1.
 CC PROSITE; PS0207; CASPASE_P10; 1.
 CC PROSITE; PS0208; CASPASE_P20; 1.
 CC PROSITE; PS0168; DED; 2.
 CC Hydrolase; Thiol protease; Apoptosis; Zymogen; Repeat.
 KW PROPEP 1 218
 FT CHAIN 219 376
 FT PROPEP 377 387
 FT CHAIN 388 480
 FT ACT_SITE 319 319
 FT ACT_SITE 362 362
 FT DOMAIN 3 80

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FT DOMAIN 101 177 DED 2.
FT CONFLICT 68 71 HISR -> PHPVG (IN REF. 4).
FT CONFLICT 94 99 DNAIS -> RQCFRL (IN REF. 4).
FT CONFLICT 96 96 A -> V (IN REF. 2).
FT CONFLICT 103 107 VMLFK -> SCSEF (IN REF. 4).
FT CONFLICT 475 475 K -> N (IN REF. 4).
SQ SEQUENCE 480 AA; 55356 MW; 045268AE3DE5ED4F CRC64;

Query Match 1.7%; Score 7; DB 1; Length 480;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 407 LRKKLFF 413
Db 472 LRKKLFF 478

RESULT 34
PHOQ_SALTY STANDARD; PRT; 487 AA.
ID PHOQ_SALTY STANDARD; PRT; 487 AA.
AC P14147; Q9L3L1;
DT 01-JAN-1990 (Rel. 13, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Virulence sensor protein phoQ (EC 2.7.3.-).
GN PHOQ OR STM1230.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14028;
RX MEDLINE=8926942; PubMed=2544889;
RA Miller S.I., Kukral A.M., Mekalanos J.J.;
RA "A two-component regulatory system (phoP phoQ) controls Salmonella
RT typhimurium virulence.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:5054-5058 (1989).
RN [2]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-313.
RC STRAIN=SL1344;
RX MEDLINE=21437654; PubMed=11553591;
RA Cano D.A., Martinez-Moya M., Pucciarelli M.G., Groisman E.A.,
RA Casadesus J., Garcia-del Portillo F.;
RA "Salmonella enterica serovar typhimurium response involved in
RT attenuation of pathogen intracellular proliferation.";
RL Infect. Immun. 69:6463-6474 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
RL Nature 413:852-856 (2001).
CC -!- FUNCTION: Member of the two-component regulatory system phoQ/phoP
CC which regulates the expression of genes involved in virulence and
CC promotes intramacrophage survival of S.typhimurium. Is required to
CC attenuate bacterial growth within fibroblast cells. PhoQ may
CC function as a membrane-associated protein kinase that
CC phosphorylates phoP in response to environmental signals.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (probable).
CC -!- SIMILARITY: Contains 1 HAMP domain.
CC -!- SIMILARITY: Contains 1 histidine kinase domain.
CC
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CC
CC -----
CC EMBL; M24424; AAA27189.1; -.
CC EMBL; AJ272210; CAB75592.1; -.
CC EMBL; AE008753; AAL20159.1; -.
CC
CC StyGene; SG10294; phoQ.
CC InterPro; IPR003594; ATPbind_ATPase.
CC InterPro; IPR004358; Bact_sens_pr_C.
CC InterPro; IPR003660; HAMP.
CC InterPro; IPR003661; His_kinA_N.
CC InterPro; IPR005467; His_kinase.
CC
CC Pfam; PF00672; HAMP; 1.
CC Pfam; PF02518; HATPase_c; 1.
CC Pfam; PF00512; Hiska; 1.
CC
CC PRINTS; PR00344; BCTRUSENSOR.
CC SMART; SM00387; HATPase_c; 1.
CC SMART; SM00388; Hiska; 1.
CC
CC PROSITE; PS50885; HAMP; 1.
CC
CC Sensory transduction; Transferase; Kinase; Phosphorylation;
KW Transmembrane; Inner membrane; Growth regulation; Virulence;
KW Complete proteome.
FT DOMAIN 1 16 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 17 37 POTENTIAL.
FT DOMAIN 38 194 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 195 215 POTENTIAL.
FT DOMAIN 216 487 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 216 266 HAMP.
FT DOMAIN 274 481 HISTIDINE KINASE.
FT MOD_RES 277 277 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT VARIANT 82 99 MISSING (IN STRAIN ATCC 10428).
FT VARIANT 442 459 MISSING (IN STRAIN ATCC 10428).
FT MUTAGEN 313 313 R->W; INCREASED ABILITY TO PROLIFERATE
FT WITHIN FIBROBLASTS.
SQ SEQUENCE 487 AA; 55466 MW; BDCFEFC56F4CA058 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 VLLSREL 34
Db 332 VLLSREL 338

RESULT 35
VRK2_MOUSE STANDARD; PRT; 503 AA.
ID VRK2_MOUSE STANDARD; PRT; 503 AA.
AC Q8BNZ1; Q8BPU8; Q8CJ46; Q91WS1; Q9CZF9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase VRK2 (EC 2.7.1.37) (Vaccinia-related
DE kinase 2).
GN VRK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6;
RX PubMed=12417526;
RA Agoulnik A.I., Lu B., Zhu Q., Truong C., Ty M.T., Arango N.,
RA Chada K.K., Bishop C.E.;
RT "A novel gene, Pog, is necessary for primordial germ cell
RT proliferation in the mouse and underlies the germ cell deficient
RT mutation, gcd.";
RL Hum. Mol. Genet. 11:3047-3053 (2002).
RN [2]

```

SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4).
 RP STRAIN=C57BL/6J; TISSUE=Embryo, Eye, and Spleen;
 RC MEDLINE=22354683; PubMed=1246881;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Otsu Y., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Iagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schrim L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guttingich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Koganaga A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertele G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Nakamura M., Sakazume N., Sato K.,
 RA Harozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa S.,
 RA Miyazaki A., Sakai K., Saeki K., Saeki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 RL [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi A.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL [4]
 RP TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
 RX MEDLINE=22666352; PubMed=12782311;
 RA Vega F.M., Gonzalo P., Gaspar M.L., Iazo P.A.;
 RT "Expression of the VRK (vaccinia-related kinase) gene family of p53
 RT regulators in murine hematopoietic development";
 RL FEBS Lett. 544:176-180 (2003).
 CC -!- FUNCTION: Probable serine/threonine kinase (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBCELLULAR LOCATION: Type IV membrane protein (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC IsoId=QB2N1-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=QB2N1-2; Sequence=VSP_008543;
 CC Note=No experimental confirmation available;
 CC PRT; 504 AA.

CC Name=3;
 CC IsoId=QB2N1-3; Sequence=VSP_008541, VSP_008542;
 CC Note=No experimental confirmation available;
 CC Name=4;
 CC IsoId=QB2N1-4; Sequence=VSP_008539, VSP_008540;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Expressed in liver, kidney and muscle. Weakly
 CC expressed in thymus, bone marrow and spleen.
 CC -!- DEVELOPMENTAL STAGE: Weakly expressed in embryo compared to VRK1
 CC and VRK3. Expressed from E10.5 to E14 in developing liver and then
 CC decreases. It increases again from E17.5 and remains thereafter.
 CC Highly expressed in hematopoietic embryonic tissues from E10.5 to
 CC E14.5. Weakly expressed in the yolk-sac.
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. VRK
 CC subfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF513620; AAN64922.1; -;
 CC EMBL; AK012664; BAB28393.1; -;
 CC EMBL; AK053297; BAC35335.1; -;
 CC EMBL; AK089825; BAC40370.1; -;
 CC EMBL; BC013520; AAI13520.1; -;
 CC HSSP; Q06486; 1CKI.
 CC MGD; MGI:1917172; Vrk2.
 CC InterPro; IPR000719; Prot kinase.
 CC ProDom; PD000001; Prot kinase; 1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
 CC PROSITE; PS00011; PROTEIN KINASE ST; 1.
 CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
 CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
 CC Transmembrane; Alternative splicing.
 CC TRANSMEM 482 502 ANCHOR FOR TYPE IV MEMBRANE PROTEIN
 CC (POTENTIAL).
 CC DOMAIN 29 313 PROTEIN KINASE (BY SIMILARITY).
 CC NP_BIND 35 61 ATP (BY SIMILARITY).
 CC ACT_SITE 166 166 BY SIMILARITY.
 CC VARSPLIC 115 115 S -> R (in isoform 4).
 CC VARSPLIC 116 503 FTID-VSP_008539.
 CC VARSPLIC 151 163 Missing (in isoform 4).
 CC VARSPLIC 151 163 /FTID=VSP_008540.
 CC VARSPLIC 151 163 LQVLEYIHENEYV -> VSLRLDITGLLDI (in
 CC isoform 3).
 CC VARSPLIC 164 503 /FTID=VSP_008541.
 CC VARSPLIC 342 390 Missing (in isoform 3).
 CC VARSPLIC 342 390 /FTID=VSP_008542.
 CC VARSPLIC 342 390 Missing (in isoform 2).
 CC CONFLICT 33 33 K -> R (IN REF. 1).
 CC CONFLICT 226 226 A -> P (IN REF. 2).
 CC CONFLICT 319 319 P -> L (IN REF. 3).
 CC CONFLICT 333 333 H -> R (IN REF. 3).
 CC SEQUENCE 503 AA; 58118 MW; 6F29E3E412ECB221 CRC64;
 CC -----
 CC Query Match 1.7%; Score 7; DB 1; Length 503;
 CC Best Local Similarity 100.0%; Pred. No. 77;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC QY 131 IGSGGFG 137
 CC DB 35 IGSGGFG 41
 CC -----
 CC RESULT 36
 CC PSD5_HUMAN
 CC ID Q8B2N1-2; Sequence=VSP_008543;
 CC AC Q16401; Q15045; STANDARD; PRT; 504 AA.

```

DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE 26S proteasome non-ATPase regulatory subunit 5 (26S proteasome
DE subunit S5B) (26S protease subunit S5 basic).
GN PSMD5 OR KIAA0072.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A., AND SEQUENCE OF 75-96; 311-337 AND 431-449.
RC TISSUE=Breast cancer;
RX MEDLINE=96007524; PubMed=7559544;
RA Deveraux Q., Jensen C., Rechsteiner M.;
RA "Molecular cloning and expression of a 26 S protease subunit enriched
RA in dileucine repeats.";
RL J. Biol. Chem. 270:23726-23729(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H.K., Moore T., Max S.J., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RA human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 2-504 FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96051398; PubMed=7584044;
RA Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S.,
RA Seki N., Kawarabayashi Y., Ishikawa K.-I., Tabata S.;
RA "Prediction of the coding sequences of unidentified human genes. II.
RA The coding sequences of 40 new genes (KIAA0041-KIAA0080) deduced by
RA analysis of cDNA clones from human cell line KG-1.";
RL DNA Res. 1:223-229(1994).
CC -!- FUNCTION: Belongs to the 26S multisubunit protease, which is
CC required for ubiquitin-dependent proteolysis. Does not bind
CC ubiquitin polymers.
CC -!- SUBUNIT: 26S protease is composed of a multicatalytic protease
CC (proteasome) and a regulatory ATPase complex. Both are
CC multisubunit structures that associate in the presence of ATP to
CC form the protease. Subunit S5B is part of the regulatory complex.
CC -!- DOMAIN: Rich in dileucine repeats, which have been implicated in
CC trafficking of a variety of transmembrane proteins.
CC -!- PTM: The N-terminus is blocked.
CC -!- SIMILARITY: BELONGS TO THE PROTEASOME SUBUNIT S5B FAMILY.
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CC EMBL; S79862; AAB35397.1; -.
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DR EMBL; BC014478; AAI14478.1; -.
DR EMBL; D31889; BAA0687.1; -.
DR Genew; HGNC:9563; PSMD5.
DR GK; Q16401; -.
DR MIM; 604452; -.
DR GO; GO:0005837; C:26S proteasome; TAS.
DR InterPro; IPR008938; ARM.
KW Proteasome.
SQ SEQUENCE 504 AA; 56195 MW; 30F31602DDF4EF89 CRC64;
Query Match 1.7%; Score 7; DB 1; Length 504;
Best Local Similarity 100.0%; Pred. No. 77; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;
Qy 329 LDAISSL 335
Db 362 LDAISSL 368
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RESULT 37
SPKD SYN3 STANDARD; PRT; 505 AA.
AC P54735;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, last sequence update)
DT 15-MAR-2004 (Rel. 43, last annotation update)
DE Serine/threonine-protein kinase D (EC 2.7.1.37).
GN SPKD OR SL0776.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=22159630; PubMed=12169951;
RA Kamei A., Yusa T., Geng X., Ikeuchi M.;
RA "Biochemical examination of the potential eukaryotic-type protein
RA kinase genes in the complete genome of the unicellular Cyanobacterium
RA synechocystis sp. PCC 6803.";
RL DNA Res. 9:71-78(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugita M., Tabata S.;
RA "Sequence analysis of the genome of the unicellular cyanobacterium
RA Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RA region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
-----
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-----
CC EMBL; AB046600; BAB17036.1; -.
CC EMBL; D64005; BAA10726.1; -.
CC FIR; S77034; S77034.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC InterPro; IPR003646; SH3_bac.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00287; SH3b; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
CC PROSITE; PSS0011; PROTEIN KINASE DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
Complete proteome.

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FT DOMAIN          9 271 PROTEIN KINASE.
FT NP BIND         15 23  ATP (BY SIMILARITY).
FT BINDING         40 40  ATP (BY SIMILARITY).
FT ACT SITE       136 136  BY SIMILARITY.
SQ SEQUENCE       505 AA; 55213 MW; C4F12A186C4D51C CRC64;

Query Match      1.7%; Score 7; DB 1; Length 505;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 GSGGFGD 138
Db 16 GSGGFGD 22

RESULT 38
VRK2 HUMAN
ID VRK2_HUMAN STANDARD; PRT; 508 AA.
AC Q86Y07; Q86Y08; Q86Y09; Q86Y10; Q86Y11; Q86Y12; Q86Y15; Q99987;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase VRK2 (EC 2.7.1.37) (Vaccinia-related
DE kinase 2).
GN VRK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RC TISSUE=Liver;
RX MEDLINE=98008921; PubMed=9344656;
RA Nezu J.-I., Oku A., Jones M.H., Shimane M.;
RT "Identification of two novel human putative serine/threonine kinases,
RT VRK1 and VRK2, with structural similarity to Vaccinia virus B1R
RT Kinase.";
RL Genomics 45:327-331(1997).
RN [2]
SEQUENCE FROM N.A. (ISOFORM 2).
RA Blanco S., Klimcakova L., Santos C., Sevilla A., Lazo P.A.;
RT "Expression of a variant isoform of the human vaccinia-related kinase
RT 2 (VRK2B) and its effects on p53 dependent transcription.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4 AND 5), AND VARIANT ILE-167.
RA Suriyaputra S.P., Sarfarazi M.;
RT "Identification of 6 different isoforms for Vaccinia-related kinase 2
RT (VRK2) gene.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Krausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buertow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";

```

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Probable serine/threonine kinase (By similarity).

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated protein.

-!- SUBCELLULAR LOCATION: Type IV membrane protein (Potential).

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=5;

Name=1;

Isoid=Q86Y07-1; Sequence=Displayed;

Name=2;

Isoid=Q86Y07-2; Sequence=VSP_008537, VSP_008538;

Note=No experimental confirmation available;

Name=3;

Isoid=Q86Y07-3; Sequence=VSP_008533;

Note=No experimental confirmation available;

Name=4; Synonyms=5;

Isoid=Q86Y07-4; Sequence=VSP_008534;

Note=No experimental confirmation available;

Name=5; Synonyms=6;

Isoid=Q86Y07-5; Sequence=VSP_008535, VSP_008536;

Note=No experimental confirmation available;

-!- TISSUE SPECIFICITY: Widely expressed. Highly expressed in fetal liver, skeletal muscle, pancreas, heart, peripheral blood leukocytes and testis.

-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. VRK subfamily.

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EMBL; AB000450; BAA19109.1; -

EMBL; AJ512204; CAD54446.2; -

EMBL; AY228367; AAO73047.1; -

EMBL; AY228368; AAO73048.1; -

EMBL; AY228369; AAO73049.1; -

EMBL; AY228370; AAO73050.1; -

EMBL; AY228371; AAO73051.1; -

EMBL; AY228372; AAO73052.1; -

EMBL; BC027854; AAH27854.1; -

HSSP; Q06486; LCKI.

Genew; HGNC:12719; VRK2.

MM; 602169; -

InterPro; IPR000719; Prot_kinase.

InterPro; IPR008271; Ser_thr_pkin_AS.

InterPro; IPR002290; Ser_thr_pkinase.

Pfam; PF00069; pkinase; 1.

ProDom; PD000001; Prot_kinase; 1.

SMART; SM00220; S_TKC_1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

KW Transferrase; Serine/threonine-protein kinase; ATP-binding; Transmembrane; Alternative splicing; Polymorphism.

TRANSMEM 487 507 ANCHOR FOR TYPE IV MEMBRANE PROTEIN (POTENTIAL).

DOMAIN 29 319 PROTEIN KINASE.

NP_BIND 35 61 ATP (BY SIMILARITY).

ACT_SITE 166 166 BY SIMILARITY.

VARSPPLIC 1 23 Missing (in isoform 3).

FT VARSPPLIC 1 118 /FTid=VSP_008533.

FT VARSPPLIC 395 396 Missing (in isoform 4).

FT VARSPPLIC 397 508 Missing (in isoform 5).

FT VARSPPLIC 395 400 ESTERRR -> GRSIGY (in isoform 2).

FT VARSPPLIC 401 508 Missing (in isoform 2).

213 VL11EL 219
|||||
322 VL11EL 328

RESULT 40
ID E2K2 HUMAN STANDARD; PRT; 551 AA.
AC P19525;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interferon-induced, double-stranded RNA-activated protein kinase
DE (SC 2.7.1.-) (Interferon-inducible RNA-dependent protein kinase) (p68
DE kinase) (PI/eif-2A protein kinase).
DE PRKR OR EIF2AK2 OR PKR.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
[1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 101-118 AND 309-325.
RP MEDLINE=90322433; PubMed=1695551;
RA Meurs E., Chong K., Galabru J., Thomas N.S.B., Kerr I.M.,
RA Williams B.R.G., Hovanessian A.G.;
RT "Molecular cloning and characterization of the human double-stranded
RT RNA-activated protein kinase induced by interferon.";
RL Cell 62:379-390(1990).
[2]
RP REVISIONS.
RA Meurs E.;
RL Submitted (XXX-1990) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP MEDLINE=92230231; PubMed=1373553;
RA Thomis D.C., Doohan J.P., Samuel C.E.;
RT "Mechanism of interferon action: cDNA structure, expression, and
RT regulation of the interferon-induced, RNA-dependent PI/eif-2 alpha
RT protein kinase from human cells.";
RL Virology 188:33-46(1992).
[4]
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RX MEDLINE=96411668; PubMed=8812437;
RA Kuhen K.L., Shen X., Carlisle E.R., Richardson A.L., Weier H.U.G.,
RA Tanaka H., Samuel C.E.;
RT "Structural organization of the human gene (PKR) encoding an
RT interferon-inducible RNA-dependent protein kinase (PKR) and
RT differences from its mouse homolog.";
RL Genomics 36:197-201(1996).
[5]
RN SEQUENCE FROM N.A.
RP Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyawaki K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
[6]
RN MUTAGENESIS, AND AUTOPHOSPHORYLATION OF THR-446 AND THR-451.
RX MEDLINE=21326157; PubMed=11337501;
RA Zhang F., Romano P.R., Nagamura-Inoue T., Tian B., Dever T.E.,
RA Mathews M.B., Ozato K., Hinnebusch A.G.;
RT "Binding of double-stranded RNA to protein kinase PKR is required for
RT dimerization and promotes critical autophosphorylation events in the
RT activation loop.";
RL J. Biol. Chem. 276:24946-24958(2001).
[7]
RN STRUCTURE BY NMR OF 1-175.
RX MEDLINE=98409549; PubMed=9736623;
RA Nandori S., Carpick B.W., Yang Y., Williams B.R., Qin J.;
RT "Structure of the double-stranded RNA-binding domain of the protein
RT kinase PKR reveals the molecular basis of its dsRNA-mediated
RT activation.";

DR TIGRFAMS: TIGR00066; g glut trans; 1.
 DR PROSITE; PS00462; G_GLU_TRANSPETIDASE; 1.
 KW Transferase; Acyltransferase; Periplasmic; Zymogen; Signal;
 KW Glutathione biosynthesis.
 FT SIGNAL 1 24
 FT CHAIN 25 376 GAMMA-GLUTAMYLTRANSFERASE LARGE CHAIN.
 FT CHAIN 377 575 GAMMA-GLUTAMYLTRANSFERASE SMALL CHAIN.
 FT BINDING 450 450 GAMMA-GLUTAMYL (POTENTIAL).
 SQ SEQUENCE 575 AA; 61301 MW; CF2EB69F02CD0201 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 575;
 Best Local Similarity 100.0%; Pred.No. 87;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 PSLGGKP 279
 |||||
 Db 547 PSLGGKP 553

RESULT 42
 LU_HUMAN
 ID LU_HUMAN STANDARD; PRT; 628 AA.
 AC P50895;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lutheran blood group glycoprotein precursor (B-CAM cell surface glycoprotein) (Auburger B antigen) (F8/G253 antigen).
 DE LU OR BCAM OR MGK19.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 [1]
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 32-67 AND 182-203.
 RC TISSUE=Placenta;
 RX MEDLINE=95296337; PubMed=7777537;
 RA Parsons S.F., Mallinson G., Holmes C.H., Houlihan J.M., Simpson K.L., Mawby W.J., Spurr N.K., Warne D., Barclay A.N., Anstee D.J.;
 RT "The Lutheran blood group glycoprotein, another member of the immunoglobulin superfamily, is widely expressed in human tissues and is developmentally regulated in human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:5496-5500(1995).
 [2]
 RN SEQUENCE OF 1-588 FROM N.A.
 RP MEDLINE=95042297; PubMed=7954395;
 RX Campbell I.G., Foulkes W.D., Senger G., Trowsdale J.,
 RA Garin-Chesa P., Rettig W.J.;
 RT "Molecular cloning of the B-CAM cell surface glycoprotein of epithelial cancers: a novel member of the immunoglobulin superfamily.";
 RL Cancer Res. 54:5761-5765(1994).
 [3]
 RN CARBOHYDRATE-LINKAGE SITE ASN-439.
 RX MEDLINE=22660472; PubMed=12754519;
 RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
 RT "Identification and quantification of N-linked glycoproteins using hydrazide chemistry, stable isotope labeling and mass spectrometry.";
 RL Nat. Biotechnol. 21:660-666(2003).
 CC -!- FUNCTION: PROBABLE RECEPTOR. MAY MEDIATE INTRACELLULAR SIGNALING.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: WIDE TISSUE DISTRIBUTION (HIGHEST IN THE PANCREAS AND VERY LOW IN BRAIN). CLOSELY ASSOCIATED WITH THE BASAL LAYER OF CELLS IN EPITHELIA AND THE ENDOTHELIUM OF BLOOD VESSEL WALLS.
 CC -!- DEVELOPMENTAL STAGE: Is under developmental control in liver and may also be regulated during differentiation in other tissues.
 CC Upregulated following malignant transformation in some cell types.
 CC -!- POLYMORPHISM: LU is responsible for the Lutheran blood group system.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
 CC -!- DATABASE: NAMB=Blood group antigen mutation database;

NOTE=Lutheran (Lu) blood group system;
 WWW="http://www.bioc.aecom.yu.edu/bgmut/lutheran.htm".
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 EMBL; X83425; CAA58449.1; -.
 EMBL; X80026; CAA56327.1; -.
 PIR; I37202; I37202.
 PIR; I38000; I38000.
 Genew; HGNC:6722; LU.
 MIM; 111200; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
 DR GO; GO:0007155; P:cell adhesion; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_C2.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00408; IGC2; 2.
 DR PROSITE; PS00835; IG_LIKE; 5.
 KW Receptor; Immunoglobulin domain; Glycoprotein; Transmembrane; Signal;
 KW Repeat; Blood group antigen.
 FT SIGNAL 1 31
 FT CHAIN 32 628 LUTHERAN BLOOD GROUP GLYCOPROTEIN.
 FT DOMAIN 32 547 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 548 568 POTENTIAL.
 FT DOMAIN 569 628 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 32 142 IG-LIKE V-TYPE 1.
 FT DOMAIN 147 257 IG-LIKE V-TYPE 2.
 FT DOMAIN 274 355 IG-LIKE C2-TYPE 1.
 FT DOMAIN 363 441 IG-LIKE C2-TYPE 2.
 FT DOMAIN 448 541 IG-LIKE C2-TYPE 3.
 FT DISULFID 53 125 PROBABLE.
 FT DISULFID 172 237 PROBABLE.
 FT DISULFID 291 337 PROBABLE.
 FT DISULFID 384 424 PROBABLE.
 FT DISULFID 473 522 PROBABLE.
 FT CARBOHYD 321 321 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 377 377 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 383 383 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 419 419 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 439 439 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 225 226 RL -> PC (IN REF. 2).
 FT CONFLICT 355 356 EL -> DV (IN REF. 2).
 SQ SEQUENCE 628 AA; 67374 MW; C89B0A4835492B1E CRC64;

Query Match 1.7%; Score 7; DB 1; Length 628;
 Best Local Similarity 100.0%; Pred.No. 94;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 GSGGFGD 138
 |||||
 Db 620 GSGGFGD 626

RESULT 43
 UL47_HSV1F
 ID UL47_HSV1F STANDARD; PRT; 664 AA.
 AC P08313;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE Virion protein UL47 (82/81 kDa tegument protein) (VMW82/81) (VP13/14).
 GN UL47.
 OS Herpes simplex virus (type 1 / strain F).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.


```
OK NCBI_TaxID=10304;
RN SEQUENCE FROM N.A.
RA MEDLINE=87141362; PubMed=3029433;
RA McKnight J.L.C., Pellett P.E., Jenkins F.J., Roizman B.;
RT "Characterization and nucleotide sequence of two herpes simplex virus
RT 1 genes whose products modulate alpha-trans-inducing factor-dependent
RT activation of alpha genes.";
RL J. Virol. 61:992-1001(1987).
CC -!- FUNCTION: MODULATOR OF ALPHA-TIF (VNM65 PHOSPHOPROTEIN) TRANS-
CC ACTIVATION. POSSIBLY UL47 MAY HAVE KINASE ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Major tegument protein of the virions.
CC -!- DEVELOPMENTAL STAGE: Expressed in the later stages of infection.
CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL47,
CC HSV-1 13, AND VZV 11.
CC
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CC
CC EMBL; M15621; AAA45767.1; -.
CC PIR; A26133; TNBE70.
CC InterPro; IPR005029; Herpes UL47.
CC Pfam; PF03362; Herpes UL47_1.
CC Transcription regulation; Trans-acting factor; Structural protein;
CC Late protein.
CC SEQUENCE 664 AA; 70526 MW; 0EALC56B1B73B4EA CRC64;
CC
CC Query Match 1.7%; Score 7; DB 1; Length 664;
CC Best Local Similarity 100.0%; Pred. No. 99;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 270 TSCPSLG 276
CC Db 656 TSCPSLG 662
CC
CC RESULT 44
CC TR2M AGRRH STANDARD; PRT; 749 AA.
CC AC Q09109;
CC DT 01-NOV-1995 (Rel. 32, Created)
CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Tryptophan 2-monooxygenase (EC 1.13.12.3).
CC GN AUX1.
CC OS Agrobacterium rhizogenes.
CC OG Plasmid pRiA4.
CC OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
CC OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
CC OX NCBI_TaxID=359;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=A4;
CC RA Camilleri C., Jouanin L.;
CC RA MEDLINE=92033088; PubMed=1932811;
CC RT "The TR-DNA region carrying the auxin synthesis genes of the
CC Agrobacterium rhizogenes agropine-type plasmid pRiA4: nucleotide
CC sequence analysis and introduction into tobacco plants.";
CC RL Mol. Plant Microbe Interact. 4:155-162(1991).
CC CC -!- CATALYTIC ACTIVITY: L-tryptophan + O(2) = indole-3-acetamide +
CC CO(2) + H(2)O.
CC -!- PATHWAY: Biosynthesis of auxins from tryptophan; first step.
CC
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CC
CC EMBL; M61151; AAA22080.1; -.
CC PIR; I39708; I39708.
CC InterPro; IPR000759; Adrndx_reductase.
CC InterPro; IPR002937; Amino_Oxidase.
CC InterPro; IPR006064; Glycosidase.
CC InterPro; IPR000205; NAD BS.
CC Pfam; PF01593; Amino oxidase; 1.
CC Pfam; PF02027; ROLB_FOLC; 1.
CC PRINTS; PR00419; ADRDXTASE.
CC Oxidoreductase; Monooxygenase; Auxin biosynthesis; Plasmid.
CC KW SEQUENCE 749 AA; 83178 MW; 8B7793970206F97B CRC64;
CC SQ
CC
CC Query Match 1.7%; Score 7; DB 1; Length 749;
CC Best Local Similarity 100.0%; Pred. No. 11e+02;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 131 IGSFGFG 137
CC Db 421 IGSFGFG 427
CC
CC RESULT 45
CC TR2M AGRT4 STANDARD; PRT; 755 AA.
CC AC P04029;
CC DT 23-OCT-1986 (Rel. 02, Created)
CC DT 23-OCT-1986 (Rel. 02, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Tryptophan 2-monooxygenase (EC 1.13.12.3).
CC GN TMS1.
CC OS Agrobacterium tumefaciens (strain Ach5), and
CC OS Agrobacterium tumefaciens.
CC OG Plasmid pTiAch5, and Plasmid pTiA6NC.
CC OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
CC OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
CC OX NCBI_TaxID=176298, 358;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=Ach5; PLASMID=pTiAch5;
CC RX MEDLINE=84207942; PubMed=6327292;
CC RA Gielen J., de Beuckeleer M., Seurinck J., Deboeck F., de Greve H.,
CC RA Lemmers M., van Montagu M., Schell J.;
CC RT "The complete nucleotide sequence of the TL-DNA of the Agrobacterium
CC tumefaciens plasmid pTiAch5.";
CC RL EMBO J. 3:835-846(1984).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RC PLASMID=pTiA6NC;
CC RX MEDLINE=84170374; PubMed=6584906;
CC RA Klee H., Montoya A., Horodyski F., Lichtenstein C., Garfinkel D.,
CC RA Fuller S., Flores C., Peschon J., Nester E., Gordon M.;
CC RT "Nucleotide sequence of the tms genes of the pTiA6NC octopine Ti
CC plasmid: two gene products involved in plant tumorigenesis.";
CC RL Proc. Natl. Acad. Sci. U.S.A. 81:1728-1732(1984).
CC CC -!- CATALYTIC ACTIVITY: L-tryptophan + O(2) = indole-3-acetamide +
CC CO(2) + H(2)O.
CC -!- PATHWAY: Biosynthesis of auxins from tryptophan; first step.
CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF ACH5.
CC -!- SIMILARITY: SIGNIFICANT HOMOLOGY TO THE ADENINE BINDING REGION OF
CC P-HYDROXYBENZOATE HYDROXYLASE FROM P. FLUORESCENS. IT SEEMS THAT
CC THIS PROTEIN BINDS ADENINE EITHER AS SUBSTRATE OR COFACTOR.
CC
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DR	InterPro; IPR002937; Amino_oxidase.
DR	InterPro; IPR006064; Glycosidase.
DR	InterPro; IPR000205; NAD_BS.
DR	Pfam; PF01593; Amino_oxidase; 1.
DR	Pfam; PF02027; RO1E_RO1C; 1.
DR	PRINTS; PR00419; ADXRDTASE.
DR	Oxidoreductase; Monooxygenase; Auxin biosynthesis; Crown gall tumor;
KW	Plasmid.
SEQUENCE	755 AA; 83972 MW; 6FA63E502343136F CRC64;
QY	131 IGSGGFG 137
DB	436 IGSGGFG 442
RESULT 47	
YQ34_MYCTU	
ID_YQ34_MYCTU	STANDARD; PRT; 778 AA.
AC	P71933;
DT	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Hypothetical PE-PGRS family protein Rv2634c/MT2712/Mb2667c.
GN	Rv2634c OR MT2712 OR MTCY441.04C OR Mb2667c.
OS	Mycobacterium tuberculosis, and
OS	Mycobacterium bovis
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC	Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX	NCBI_TaxID=1773, 1765;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	SPECIES=M.tuberculosis; STRAIN=H37Rv;
RX	MEDLINE=98295987; PubMed=9634230;
RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA	Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA	Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA	Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA	Hornby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA	Oliver S., Osborne J., Quail M.A., Rajadream M.A., Rogers J.,
RA	Rutler S., Seeger K., Skelton S., Squares S., Squares R.,
RA	Sulston J.B., Taylor K., Whitehead S., Barrell B.G.;
RA	"Deciphering the biology of Mycobacterium tuberculosis from the
RT	complete genome sequence."
RL	Nature 393:537-544(1998).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX	MEDLINE=22206494; PubMed=12218036;
RA	Flieschmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA	Peterson J.F., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA	Kolony J.J., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA	Delcher A., Uitterback T., Weidman J., Khouri E., Gill J., Mikula A.,
RA	Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RA	"Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT	laboratory strains."
RL	J. Bacteriol. 184:5479-5490(2002).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	SPECIES=M.bovis; STRAIN=AF2122/97;
RX	MEDLINE=22709107; PubMed=12789572;
RA	Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA	Pyor M., Duthey S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA	Harris B., Atkin R., Doggett S., Mayes R., Keating L., Wheeler P.R.,
RA	Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RA	"the complete genome sequence of Mycobacterium bovis."
RT	Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003)
CC	-1- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
CC	SUBFAMILY.

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DR EMBL; Z80225; CAB02341.1; -.
DR EMBL; AE007103; AAK47026.1; ALT_INIT.
DR EMBL; BX248343; CAD94852.1; -.
DR PIR; F70963; F70963.
DR TIGR; MT2712; -.
DR TubercuList; Rv2634c; -.
DR InterPro; IPR000084; PE_region.
DR Pfam; PF00934; PE; 1.
DR ProDom; PD001223; PE_region; 1.
DR KW Hypothetical protein; Complete proteome.
FT CONFLICT 51 51 V -> L (IN REF. 2).
FT CONFLICT 63 63 Q -> H (IN REF. 2).
FT CONFLICT 274 274 A -> T (IN REF. 2).
SQ SEQUENCE 778 AA; 63131 MW; DAB20FE5BE4999E7 CRC64;

Query Match 1.7%; Score 7; DB 1; Length 778;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 IGSFGFG 137
|||||
DB 223 IGSFGFG 229

RESULT 48

HIFA_XENLA
ID HIFA_XENLA STANDARD; PRT; 805 AA.
AC Q918A9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha).
GN HIFA.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1] SEQUENCE FROM N.A.
RA Kietzmann T.;
RT "Cloning and expression of the Xenopus laevis hypoxia inducible factor
1 alpha homologue";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Functions as a master transcriptional regulator of the
CC adaptive response to hypoxia. Binds to core DNA sequence 5'-
CC [AG]CGTG-3' within the hypoxia response element (HRE) of target
CC gene promoters. Activation requires recruitment of transcriptional
CC coactivators (By similarity).
CC -!- SUBUNIT: Efficient DNA binding requires heterodimerization of an
CC alpha and a beta/ARNT subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic in normoxia, nuclear
CC translocation in response to hypoxia (By similarity).
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC
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DR EMBL; AJ277829; CAB96628.1; -.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR001321; Hypoxindf1A.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS_domain.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR PRINTS; PR01080; HYPOXIAIF1A.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS00888; HLH; FALSE_NEG.
DR PROSITE; PS0112; PAS; 2.
KW Transcription regulation; Activator; Nuclear protein; DNA-binding;
KW Repeat.
FT DNA_BIND 17 30 BASIC DOMAIN.
FT DOMAIN 31 71 HELIX-LOOP-HELIX MOTIF.
FT DOMAIN 85 157 PAS 1.
FT DOMAIN 229 300 PAS 2.
FT DOMAIN 303 346 PAC.
SQ SEQUENCE 805 AA; 90964 MW; BABFA0BD6B44FF3B CRC64;

Query Match 1.7%; Score 7; DB 1; Length 805;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 LRTFDQL 329
|||||
DB 570 LRTFDQL 576

RESULT 49

CAPP_SYNEL
ID CAPP_SYNEL STANDARD; PRT; 1011 AA.
AC Q34QB2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase) (PEPC).
GN PPC OR SVPERC OR PLL1912.
OS Synechococcus elongatus (Thermosynechococcus elongatus), and
OS Synechococcus vulcanus (Thermosynechococcus vulcanus).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32046; 32053;
RN [1] SEQUENCE FROM N.A.
RC SPECIES=S.elongatus; STRAIN=BP-1;
RX MEDLINE=2225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriiguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Makazaki N.,
RA Shimpou S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
Thermosynechococcus elongatus BP-1";
RL DNA Res. 9:123-130(2002).
RN [2] SEQUENCE FROM N.A.
RC SPECIES=S.vulcanus;
RX Chen L.M., Omiya T., Hata S., Inoue Y., Izui K.;
RT "Molecular characterization of Synechococcus vulcanus
phosphoenolpyruvate carboxylase";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Through the carboxylation of phosphoenolpyruvate (PEP)
CC it forms oxaloacetate, a four-carbon dicarboxylic acid source for
CC the tricarboxylic acid cycle.
CC -!- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
CC phosphoenolpyruvate + CO(2).
CC -!- PATHWAY: Tricarboxylic acid cycle.
CC -!- SIMILARITY: Belongs to the PEPCase family.
CC
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us-09-961-201a-1.oligo.rsp

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CC -----

DR EMBL; AP005375; BAC09464.1; -
DR EMBL; AB057454; BAB64533.1; -
DR HAMAP; MF 00595; -; 1.
DR InterPro; IPR001449; PEPcase.
DR Pfam; PF00311; PEPcase; 1.
DR PRINTS; PR00150; PEPARBXLASE
DR PROSITE; PS00781; PEPcase_1; FALSE_NEG.
DR PROSITE; PS00393; PEPcase_2; 1.
KW Lyase; Carbon dioxide fixation; Tricarboxylic acid cycle;
KW Complete proteome.
FT ACT_SITE 207 BY SIMILARITY.
FT ACT_SITE 558 BY SIMILARITY.
FT ACT_SITE 658 BY SIMILARITY.
SQ SEQUENCE 1011 AA; 116426 MW; 0A11D4D01FE9E7FE CRC64;

Query Match 1.7%; Score 7; DB 1; Length 1011;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 RLRLVEE 19
Db 27 RLRLVEE 33

RESULT 50

UL70_HCMVA STANDARD; PRT; 1062 AA.
ID UL70_HCMVA
AC P17149;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Helicase/primase complex protein (Probable DNA replication protein
DE UL70).
GN UL70.
OS Human cytomegalovirus (strain AD169).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10360;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90269039; PubMed=2161319;
RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
RA Hornell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,
RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
RT "Analysis of the protein-coding content of the sequence of human
RT cytomegalovirus strain AD169."
RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
CC -!- FUNCTION: Involved in DNA replication.
CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL52,
CC EBV-1 7, EBV BSLF1, HVS-1 56, HCMV UL70 AND VZV 6.
CC -----
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CC -----
DR EMBL; X17403; CAA35386.1; -
DR PIR; S09834;
DR InterPro; IPR004340; UL52 UL70.
DR Pfam; PF03121; UL52 UL70; 1.
KW DNA replication.
SQ SEQUENCE 1062 AA; 120925 MW; F3B8DBC29857524F CRC64;

Query Match 1.7%; Score 7; DB 1; Length 1062;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 298 VASTSPE 304
Db 604 VASTSPE 610
Search completed: August 3, 2004, 09:09:54
Job time : 16 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 09:06:52 ; Search time 39 Seconds
(without alignments)
3365.527 Million cell updates/sec

Title: US-09-961-201a-1

Perfect score: 416

Sequence: 1 MDEADRLRLRCRLALVEEL.....YKMPGCFNFKKLFFKTS 416

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database :

SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriapi.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	6.7	393	11	Q9R0S9
2	28	6.7	453	11	Q8C3Q0
3	28	6.7	454	11	Q9JHK1
4	28	6.7	454	11	Q9R0T0
5	28	6.7	454	11	Q8C3Q9
6	26	6.2	383	11	Q99M88
7	20	4.8	177	11	Q920G4
8	20	4.8	229	11	Q7TQC1
9	17	4.1	403	13	Q90WU0
10	11	2.6	280	13	Q8JGM9
11	11	2.6	280	13	Q8JG42
12	11	2.6	280	13	Q8JIS9
13	11	2.6	282	13	Q98JI8
14	11	2.6	283	13	Q934I7
15	11	2.6	290	13	Q8JIS8
16	11	2.6	293	5	Q8I9V7

RESULT 1

Q9R0S9 PRELIMINARY; PRT; 393 AA.
ID Q9R0S9
AC Q9R0S9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Caspase9S.
GN CASP9.

ALIGNMENTS

17	11	2.6	299	5	Q8I955
18	11	2.6	318	13	Q9IB65
19	11	2.6	400	5	Q8ITP2
20	10	2.4	303	11	Q88550
21	10	2.4	308	5	Q9NH9
22	10	2.4	308	5	Q9VET9
23	10	2.4	476	13	Q9IBJ3
24	10	2.4	520	13	Q9IB62
25	10	2.4	522	4	Q8IUP5
26	9	2.2	370	5	Q22518
27	9	2.2	481	11	Q8I2G4
28	9	2.2	1121	10	Q942F3
29	9	2.2	1164	9	Q9LJF3
30	8	1.9	145	9	Q8LIT85
31	8	1.9	158	10	Q8H436
32	8	1.9	165	17	Q970W7
33	8	1.9	266	16	Q82TV7
34	8	1.9	272	16	Q7V7P6
35	8	1.9	272	16	Q7U6Q4
36	8	1.9	324	16	Q8YAX5
37	8	1.9	368	16	Q9XAC4
38	8	1.9	372	16	Q9KUW7
39	8	1.9	378	16	Q8FXG8
40	8	1.9	399	13	Q9IB63
41	8	1.9	415	13	Q801M6
42	8	1.9	419	13	Q7ZXD2
43	8	1.9	423	13	Q9IB67
44	8	1.9	618	2	Q8KFX0
45	8	1.9	752	5	Q21026
46	8	1.9	758	5	Q22203
47	8	1.9	787	10	O48847
48	8	1.9	794	5	O18107
49	8	1.9	975	5	Q9VAX8
50	8	1.9	1031	5	Q962H8
51	8	1.9	1393	16	Q822J2
52	8	1.9	1791	16	O8ABE6
53	7	1.7	87	9	Q854Q9
54	7	1.7	91	2	Q9EXM1
55	7	1.7	93	16	Q7UTA8
56	7	1.7	98	16	Q8YLM1
57	7	1.7	111	2	Q9Z4C6
58	7	1.7	116	4	Q7Z5Z7
59	7	1.7	121	11	Q8BG00
60	7	1.7	121	16	Q99SC1
61	7	1.7	123	2	Q9ZAN6
62	7	1.7	126	8	Q9B4Y3
63	7	1.7	129	5	Q9N9C1
64	7	1.7	131	10	Q7XQY4
65	7	1.7	135	2	Q53304
66	7	1.7	138	16	Q8EQK6
67	7	1.7	141	10	Q9S7T2
68	7	1.7	143	9	Q857D0
69	7	1.7	143	16	Q83DN9
70	7	1.7	152	16	Q7U4I3
71	7	1.7	153	12	Q91MM8
72	7	1.7	153	12	Q8JTP4
73	7	1.7	153	12	Q8JUT3
74	7	1.7	156	13	Q7ZW78
75	7	1.7	156	16	Q8DC79

Q8I955 spodoptera
Q9IB65 xenopus lae
Q8ITP2 branchiosto
Q88550 rattus norv
Q9NH9 drosophila
Q9VET9 drosophila
Q9IBJ3 brachydanio
Q9IB62 xenopus lae
Q8IUP5 homo sapien
Q22518 caenorhabdi
Q8I2G4 mus musculu
Q942F3 oryza sativ
Q9LJF3 arabidopsis
Q8LIT85 vibriophag
Q8H436 oryza sativ
Q970W7 sulfolobus
Q82TV7 nitrosomona
Q7V7P6 prochloroco
Q7U6Q4 synechococc
Q8YAX5 bruceella me
Q9XAC4 streptomyce
Q9KUW7 vibrio chol
Q8FXG8 bruceella su
Q9IB63 xenopus lae
Q801M6 xenopus lae
Q7ZXD2 xenopus lae
Q9IB67 xenopus lae
Q8KFX0 saccharopol
Q21026 caenorhabdi
Q22203 caenorhabdi
O48847 arabidopsis
O18107 caenorhabdi
Q9VAX8 drosophila
Q962H8 toxoplasma
Q822J2 chlamydophi
Q8ABE6 bacteroides
Q854Q9 mycobacteri
Q9EXM1 escherichia
Q7UTA8 rhodopirell
Q8YLM1 anabaena sp
Q9Z4C6 salmonella
Q7Z5Z7 homo sapien
Q8BG00 mus musculu
Q99SC1 bradyrhizob
Q9ZAN6 comamonas s
Q9B4Y3 graomys gri
Q9N9C1 leishmania
Q7XQY4 oryza sativ
Q53304 mycoplasma
Q8EQK6 oceanobacil
Q9S7T2 oryza sativ
Q857D0 mycobacteri
Q83DN9 coxiella bu
Q7U4I3 synechococc
Q91MM8 lumpy skin
Q8JTP4 lumpy skin
Q8JUT3 lumpy skin
Q7ZW78 brachydanio
Q8DC79 vibrio vuln

RL	Biochem. J.	360	49-56(2001).
DR	EMBL:	AF262319;	AAF85658.1; -.
DR	EMBL:	AF271996;	AAF76217.1; -.
DR	EMBL:	AF286006;	AAF99705.1; -.
DR	EMBL:	AF308469;	AAK35159.1; -.
DR	EMBL:	AY027667;	AAK26235.1; -.
DR	HSSP:	P42574;	1PAU.
DR	MEROPS:	C14.010;	-.
DR	GO:	GO:0005622;	C:intracellular; IEA.
DR	GO:	GO:0016329;	F:apoptosis regulator activity; IEA.
DR	GO:	GO:0030693;	F:caspase activity; IEA.
DR	GO:	GO:0006915;	P:apoptosis; IEA.
DR	GO:	GO:0006508;	P:proteolysis and peptidolysis; IEA.
DR	InterPro:	IPR001315;	CARD.
DR	InterPro:	IPR002138;	ICE_p10.
DR	InterPro:	IPR001309;	ICE_P20.
DR	InterPro:	IPR002398;	Peptidase_C14.
DR	Pfam:	PF00619;	CARD; 1.
DR	Pfam:	PF00656;	Peptidase_C14; 1.
DR	PRINTS:	PR00376;	ILIIBENZYME.
DR	SMART:	SM00114;	CARD; 1.
DR	SMART:	SM00115;	CASC; 1.
DR	PROSITE:	PS50209;	CARD; 1.
DR	PROSITE:	PS01122;	CASPASE_CYS; 1.
DR	PROSITE:	PS01121;	CASPASE_HIS; 1.
DR	PROSITE:	PS50207;	CASPASE_P10; 1.
DR	PROSITE:	PS50208;	CASPASE_P20; 1.
DR	SEQUENCE	454 AA;	50399 MW; 501623B29E6DE6FC CRC64;
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Query Match	6.7%; Score 28; DB 11; Length 454;		
Best Local Similarity	100.0%; Pred.No. 2.6e-20;		
Matches	28; Conservative	0; Mismatches	0; Indels 0; Gaps
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Qy	272	CPSLGGKPKLFFIQACGGEQKHGHFEVA	299
Dd	310	CPSLGGKPKLFFIQACGGEQKHGHFEVA	337
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RESULT 4			
Q9ROT0			
ID	Q9ROT0	PRELLIMINARY;	PRT; 454 AA.
AC	Q9ROT0;		
DT	01-MAY-2000	(TEMBLrel. 13, Created)	
DT	01-MAY-2000	(TEMBLrel. 13, Last sequence update)	
DT	01-OCT-2003	(TEMBLrel. 25, Last annotation update)	
DE	Caspase9.		
GN	CASP9.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI_TaxID=10090;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20001956; PubMed=10529400;		
RA	Fujita E., Jinbo A., Matuzaki H., Konishi H., Kikkawa U., Momoi T.;		
RT	"Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9";		
RL	Biochem. Biophys. Res. Commun. 264:550-555(1999).		
DR	EMBL:	AB019600;	BAA86895.1; -.
DR	PfR:	JC7123;	JC7123.
DR	HSSP:	P42574;	1PAU.
DR	MEROPS:	C14.010;	-.
DR	MGD:	MGI:1277950;	Casp9.
DR	GO:	GO:0005622;	C:intracellular; IEA.
DR	GO:	GO:0016329;	F:apoptosis regulator activity; IEA.
DR	GO:	GO:0030693;	F:caspase activity; IEA.
DR	GO:	GO:0006915;	P:apoptosis; IEA.
DR	GO:	GO:0006508;	P:proteolysis and peptidolysis; IEA.
DR	InterPro:	IPR001315;	CARD.
DR	InterPro:	IPR002138;	ICE_p10.
DR	InterPro:	IPR001309;	ICE_P20.
DR	InterPro:	IPR002398;	Peptidase_C14.
DR	Pfam:	PF00619;	CARD; 1.

```
RESULT 6
Q99M88 PRELIMINARY; PRT; 383 AA.
AC Q99M88, 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-9 CTD isoform.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21192275; PubMed=11278518;
RA Angelastro J.M., Moon N.Y., Liu D.X., Yang A.-S., Greene L.A.,
RA Franke T.F.;
RT "Characterization of a Novel Caspase-9 Isoform in Rat That Inhibits
RT Apoptosis.";
RL J. Biol. Chem. 276:12190-12200(2001).
DR EMBL; AY008275; AAC21690.1; -.
DR HSP; P42574; IPAU.
DR MEROPS; C14.0107; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILLICENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02008; CASPASE_P20; 1.
SQ SEQUENCE 383 AA; 43319 MW; 3C5D217C3100FF25 CRC64;

Query Match 6.2%; Score 26; DB 11; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.9e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 VVILSHGCOASHLQFPFGVYGTDC 256
Db 269 VVILSHGCOASHLQFPFGVYGTDC 294

RESULT 7
Q920G4 PRELIMINARY; PRT; 177 AA.
AC Q920G4, 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Caspase-9 short form.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA Cao G., Chen D., Ma L., Graham S.H., Chen J.;
RT "Cloning and Characterization of Rat Caspase-9: Implication for a Role
RT in Neuronal Cell Death During Brain Development and Transient Cerebral
RT Ischemia.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF293333; AAK97066.1; -.

RESULT 8
Q7TQCI PRELIMINARY; PRT; 229 AA.
AC Q7TQCI, 2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 25 kDa caspase-9 dominant negative protein.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA Cao G., Wu S., Sheng L., Graham S.H., Zhou Z., Chen J.;
RT "Molecular cloning and characterization of three caspase-9 dominant
RT negative forms in rats.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV124461; AAM92272.1; -.
DR EMBL; AV124461; AAM92272.1; -.
SQ SEQUENCE 229 AA; 25194 MW; 87C293AF139F3B23 CRC64;

Query Match 4.8%; Score 20; DB 11; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 MIEDIQAGSGSRDQARQL 58
Db 39 MIEDIQAGSGSRDQARQL 58

RESULT 9
Q90WU0 PRELIMINARY; PRT; 403 AA.
AC Q90WU0, 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 9 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Barton S., Bridgman J.T., Johnson A.L.;
RT "Caspase-8 and -9 expression in the hen ovary.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057940; AAL23701.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0005486; F:binding; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
```

```
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR001315; CARD.
DR Pfam; PF00619; CARD; 1.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS0209; CARD; 1.
SQ SEQUENCE 177 AA; 19700 MW; E9DCDA77156AD748 CRC64;

Query Match 4.8%; Score 20; DB 11; Length 177;
Best Local Similarity 100.0%; Pred. No. 3e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 MIEDIQAGSGSRDQARQL 58
Db 39 MIEDIQAGSGSRDQARQL 58

RESULT 8
Q7TQCI PRELIMINARY; PRT; 229 AA.
AC Q7TQCI, 2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 25 kDa caspase-9 dominant negative protein.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA Cao G., Wu S., Sheng L., Graham S.H., Zhou Z., Chen J.;
RT "Molecular cloning and characterization of three caspase-9 dominant
RT negative forms in rats.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV124461; AAM92272.1; -.
DR EMBL; AV124461; AAM92272.1; -.
SQ SEQUENCE 229 AA; 25194 MW; 87C293AF139F3B23 CRC64;

Query Match 4.8%; Score 20; DB 11; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 MIEDIQAGSGSRDQARQL 58
Db 39 MIEDIQAGSGSRDQARQL 58

RESULT 9
Q90WU0 PRELIMINARY; PRT; 403 AA.
AC Q90WU0, 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 9 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Barton S., Bridgman J.T., Johnson A.L.;
RT "Caspase-8 and -9 expression in the hen ovary.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057940; AAL23701.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0005486; F:binding; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
```


DR GO: GO:0006915; P:apoptosis; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR001315; CARD.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002398; Peptidase_C14.
 DR Pfam: PF00619; CARD; 1.
 DR Pfam: PF00656; Peptidase_C14; 1.
 DR PRINTS: PR00376; IL1BCENZYM.
 DR SMART: SM00115; CASC; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS0207; CASPASE_P10; 1.
 DR PROSITE: PS0208; CASPASE_P20; 1.
 DR PROSITE: PS0215; MITOCH_CARRIER; 1.
 FT NON TER 1
 SQ SEQUENCE 403 AA; 44913 MW; 0F1B40C3E6594FC4 CRC64;
 Query Match 4.1%; Score 17; DB 13; Length 403;
 Best Local Similarity 100.0%; Pred. No. 9.7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 277 GKPFLFFIQACGGEQXD 293
 Db 264 GKPFLFFIQACGGEQXD 280
 RESULT 10
 Q8JGM9 PRELIMINARY; PRT; 280 AA.
 AC Q8JGM9;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Caspase 3-like.
 GN CASP3.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hewitt J.E., Bolland D.J.;
 RT "Sequence comparisons of an evolutionary chromosomal breakpoint in human, mouse and pufferfish";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A102865; AAM48291.1; -;
 DR GO: GO:0030693; F:caspase activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR Pfam: PF00656; Peptidase_C14; 1.
 DR PRINTS: PR00376; IL1BCENZYM.
 DR SMART: SM00115; CASC; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS0207; CASPASE_P10; 1.
 DR PROSITE: PS0208; CASPASE_P20; 1.
 SQ SEQUENCE 280 AA; 30538 MW; 4D58912159A37347 CRC64;

Query Match 2.6%; Score 11; DB 13; Length 280;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPFLFFIQAC 287
 Db 159 GKPFLFFIQAC 169

RESULT 11
 Q8JG42 PRELIMINARY; PRT; 280 AA.
 AC Q8JG42;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Caspase 3.
 GN CASP3.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Grewal P.K., van Deutekom J.C., Mills K.A., Lemmers R.J.,
 RA Mathews K.D., Frants R.R., Hewitt J.E.;
 RT "The mouse homolog of FRG1, a candidate gene for FSHD, maps proximal to the myodystrophy mutation on chromosome 8";
 RL Mamm. Genome 8:394-398(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Grewal P.K., Todd L.C., van der Maarel S., Frants R.R., Hewitt J.E.;
 RT "FRG1, a gene in the FSH muscular dystrophy region on human chromosome 4q35, is highly conserved in vertebrates and invertebrates";
 RL Gene 216:13-19(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Bolland D.J., Hewitt J.E.;
 RT "Intron loss in the SART1 genes of Fugu rubripes and Tetraodon nigroviridis";
 RL Gene 271:43-49(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Bolland D.J., van Geel M., Carim Todd L., Grewal P.K., Beck A.F.,
 RA van der Maarel M. Sr., Frants R.R., de Jong P.J., Hewitt J.E.;
 RT "Sequence comparisons of an Evolutionary Chromosomal Breakpoint in Human, Mouse and Puffer Fish";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF042797; AAM43816.1; -;
 DR GO: GO:0030693; F:caspase activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR Pfam: PF00656; Peptidase_C14; 1.
 DR PRINTS: PR00376; IL1BCENZYM.
 DR SMART: SM00115; CASC; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS0207; CASPASE_P10; 1.
 DR PROSITE: PS0208; CASPASE_P20; 1.
 SQ SEQUENCE 280 AA; 30524 MW; 4F2D91245A7EC642 CRC64;
 Query Match 2.6%; Score 11; DB 13; Length 280;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 277 GKPFLFFIQAC 287
 Db 159 GKPFLFFIQAC 169

RESULT 12
 Q8JIS9 PRELIMINARY; PRT; 280 AA.
 ID Q8JIS9
 AC Q8JIS9;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 3b.
OS Eukaryotas latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20211495; PubMed=10747068;
RA Naruse K., Fukumachi S., Mitani H., Kondo M., Matsuoka T., Kondo S.,
RA Hanamura N., Morita Y., Hasegawa K., Nishigaki R., Shimada A.,
RA Wada H., Kusakabe T., Suzuki N., Kinoshita M., Kanamori A., Terado T.,
RA Kimura H., Nonaka M., Shima A.;
RT "A Detailed Linkage Map of Medaka, *Oryzias latipes*: Comparative
RT Genomics and Genome Evolution.";
RL Genetics 154:1773-1784(2000).
DR EMBL; AB032608; F:caspase activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILIBCENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 280 AA; 31168 MW; 5095512F1E485542 CRC64;

Query Match 2.6%; Score 11; DB 13; Length 280;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 277 GKPKLFFFIQAC 287
Db 160 GKPKLFFFIQAC 170

RESULT 13
Q98UI8
ID Q98UI8 PRELIMINARY; PRT; 282 AA.
AC Q98UI8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-3.
GN CASP3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RN SEQUENCE FROM N.A.
RA Yabu T., Okazaki T., Yamashita M.;
RT "Molecular Cloning and Gene Expression of Zebrafish Caspase Related to
RT Mammalian Caspase-3";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047003; BAB32409.1; -.
DR HSSP; P42574; IPAU.
DR MEROPS; C14.003; -.
DR ZFIN; ZDB-GENE-011210-1; casp3.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase C14.

DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILIBCENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 282 AA; 31522 MW; 13C3454F5E09932B CRC64;

Query Match 2.6%; Score 11; DB 13; Length 282;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 277 GKPKLFFFIQAC 287
Db 156 GKPKLFFFIQAC 166

RESULT 14
Q93417
ID Q93417 PRELIMINARY; PRT; 283 AA.
AC Q93417;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20149872; PubMed=10684799;
RA Johnson A.L., Bridgham J.T.;
RT "Caspase-3 and -6 expression and enzyme activity in hen granulosa
RT cells.";
RL Biol. Reprod. 62:589-598(2000).
DR EMBL; AF083029; AAC32602.1; -.
DR HSSP; P42574; IPAU.
DR MEROPS; C14.003; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILIBCENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 283 AA; 31675 MW; 161242DDEFD4DC4F CRC64;

Query Match 2.6%; Score 11; DB 13; Length 283;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 277 GKPKLFFFIQAC 287
Db 161 GKPKLFFFIQAC 171

RESULT 15
Q8JIS8
ID Q8JIS8 PRELIMINARY; PRT; 290 AA.
AC Q8JIS8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 3a.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20211495; PubMed=10747068;
RA Naruse K., Fukamachi S., Mitani H., Kondo M., Matsuoka T., Kondo S.,
RA Hanamura N., Morita Y., Hasegawa K., Nishigaki R., Shimada A.,
RA Wada H., Kusakabe T., Suzuki N., Kinoshita M., Kanamori A., Terado T.,
RA Kimura H., Nonaka M., Shima A.,
RA "A Detailed Linkage Map of Medaka, Oryzias latipes: Comparative
RT Genomics and Genome Evolution.";
RL Genetics 154:1773-1784(2000).
DR EMBL; AB032609; BAC00949.1; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 290 AA; 32686 MW; D8C3BC00D32E8A6C CRC64;

Query Match 2.6%; Score 11; DB 13; Length 290;
Best Local Similarity 100.0%; Pred.No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFIQAC 287
DB 166 GKPKLFFIQAC 176

RESULT 16
QY 277 GKPKLFFIQAC 287
DB 166 GKPKLFFIQAC 176

ID Q8I9V7 PRELIMINARY; PRT; 293 AA.
AC Q8I9V7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-1.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22358983; PubMed=12324475;
RA Pei Z., Reske G., Huang Q., Hammock B.D., Qi Y., Chejanovsky N.;
RT "Characterization of the Apoptosis Suppressor Protein P49 from the
RT Spodoptera littoralis Nucleopolyhedrovirus.";
RL J. Biol. Chem. 277:48677-48684(2002).
DR EMBL; AF448494; AA86250.1; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 293 AA; 33340 MW; 8184A9FD910D7E34 CRC64;
```

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Query Match 2.6%; Score 11; DB 5; Length 293;
Best Local Similarity 100.0%; Pred.No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFIQAC 287
DB 165 GKPKLFFIQAC 175

RESULT 17
QY 277 GKPKLFFIQAC 287
DB 165 GKPKLFFIQAC 175

ID Q8I955 PRELIMINARY; PRT; 299 AA.
AC Q8I955;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Effector caspase.
OS Spodoptera littoralis (Egyptian cotton leafworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Amphipyridae; Spodoptera.
OX NCBI_TaxID=7109;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Q., Gershbarg E., Qi Y., Chejanovsky N.;
RT "Suppression of apoptosis in Spodoptera littoralis SL2 cells by the
RT baculovirus proteins P35 and P49.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF548387; AAO16241.1; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 299 AA; 33442 MW; B13AF2C1A6BD409D CRC64;

Query Match 2.6%; Score 11; DB 5; Length 299;
Best Local Similarity 100.0%; Pred.No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFIQAC 287
DB 168 GKPKLFFIQAC 178

RESULT 18
QY 277 GKPKLFFIQAC 287
DB 168 GKPKLFFIQAC 178

ID Q9IB65 PRELIMINARY; PRT; 318 AA.
AC Q9IB65;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-7.
DR CASPASE-7.
GN Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yacita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family.";
```

RL J. Biol. Chem. 275:10484-10491 (2000).

DR EMBL; AB0381170; BAA394748.1; --

DR HSSP; P42574; 1PAU.

DR MEROPS; C14.004; --

DR GO; GO:0030693; F:caspase activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR002138; ICE p10.

DR InterPro; IPR001309; ICE p20.

DR InterPro; IPR002398; Peptidase C14.

DR Pfam; PF00656; Peptidase C14; 1.

DR PRINTS; PR00376; IL1BCENZYM.

DR SMART; SM00115; CASC; 1.

DR PROSITE; PS01122; CASPASE_CYS; 1.

DR PROSITE; PS01121; CASPASE_HIS; 1.

DR PROSITE; PS50207; CASPASE_P10; 1.

DR PROSITE; PS50208; CASPASE_P20; 1.

SQ SEQUENCE 318 AA; 35397 MW; 6BEC6684AF86A128 CRC64;

Query Match 2.6%; Score 11; DB 13; Length 318;

Best Local Similarity 100.0%; Pred. No. 0.017;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFIQAC 287

Db 187 GKPKLFFIQAC 197

RESULT 19

Q8ITP2

ID Q8ITP2 PRELIMINARY; PRT; 400 AA.

AC Q8ITP2;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE AmphicASP-6.

OS Branchiostoma floridae (Florida lancelet) (Amphioxus).

OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;

OC Branchiostoma.

OX NCBI_TaxID=7739;

RN [1]

RP SEQUENCE FROM N.A.

RA Bayasas J.R., Yuste V.J., Benito E., Garcia-Fernandez J.,

Comella J.X.;

RT "Isolation of AmphicASP-6, an amphioxus (Branchiostoma floridae)

caspase-6 homolog containing a Pyrin prodomain."

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF412336; AAN45850.1; --

DR GO; GO:0030693; F:caspase activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR002138; ICE p10.

DR InterPro; IPR001309; ICE p20.

DR InterPro; IPR002398; Peptidase C14.

DR Pfam; PF00656; Peptidase C14; 1.

DR PRINTS; PR00376; IL1BCENZYM.

DR SMART; SM00115; CASC; 1.

DR PROSITE; PS01122; CASPASE_CYS; 1.

DR PROSITE; PS01121; CASPASE_HIS; 1.

DR PROSITE; PS50207; CASPASE_P10; 1.

DR PROSITE; PS50208; CASPASE_P20; 1.

SQ SEQUENCE 400 AA; 44309 MW; 5C3B1B813E73DFAE CRC64;

Query Match

Best Local Similarity 2.6%; Score 11; DB 5; Length 400;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 GKPKLFFIQAC 287

Db 260 GKPKLFFIQAC 270

RESULT 20

O88550

ID O88550 PRELIMINARY; PRT; 303 AA.

AC O88550;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Caspase-7.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RA Forghani F., Roy S.;

RT "Rat caspase-7 sequence."

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF072124; AAC24011.1; --

DR HSSP; P42574; 1PAU.

DR MEROPS; C14.004; --

DR GO; GO:0030693; F:caspase activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR002138; ICE p10.

DR InterPro; IPR001309; ICE p20.

DR InterPro; IPR002398; Peptidase C14.

DR Pfam; PF00656; Peptidase C14; 1.

DR PRINTS; PR00376; IL1BCENZYM.

DR SMART; SM00115; CASC; 1.

DR PROSITE; PS01122; CASPASE_CYS; 1.

DR PROSITE; PS01121; CASPASE_HIS; 1.

DR PROSITE; PS50207; CASPASE_P10; 1.

DR PROSITE; PS50208; CASPASE_P20; 1.

SQ SEQUENCE 303 AA; 34324 MW; A71728754BF199DD CRC64;

Query Match

Best Local Similarity 2.4%; Score 10; DB 11; Length 303;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPCLFFIQAC 287

Db 177 KPCLFFIQAC 186

RESULT 21

Q9NH9

ID Q9NH9 PRELIMINARY; PRT; 308 AA.

AC Q9NH9;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Caspase 6-like protein Bg2.

GN DRCAY OR CG14902.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RA Zhou J., Steller H.;

RT "Bg2, a potential Drosophila homologue of Caspase 6."

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF222007; AAF44327.1; --

DR HSSP; P42574; 1PAU.

DR MEROPS; C14.022; --

DR FlyBase; FBgn0028381; decay.

DR GO; GO:0005737; C:cytoplasm; IDA.

DR GO; GO:0004208; F:caspase-3 activity; IDA.

DR GO; GO:0004207; F:effector caspase activity; NAS.

DR GO; GO:0006915; P:apoptosis; IMP.

DR InterPro; IPR002138; ICE p10.

DR InterPro; IPR001309; ICE p20.

DR InterPro; IPR002398; Peptidase C14.

DR Pfam; PF00656; Peptidase C14; 1.

DR PRINTS; PR00376; IL1BCENZYM.

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DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01127; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50209; CASPASE_P20; 1.
SQ SEQUENCE 308 AA; 34897 MW; E3FDAB05FEC7E93 CRC64;

Query Match 2.4%; Score 10; DB 5; Length 308;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPXLFFFIQAC 287
Db 162 KPXLFFFIQAC 171

RESULT 22
Q9VET9
ID Q9VET9 PRELIMINARY; PRT; 308 AA.
AC Q9VET9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Decay protein (AT03047p).
GN DSCAY OR CG14902.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-pfaunkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).

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RP SEQUENCE FROM N.A.
RX MEDLINE=99452973; PubMed=10521468;
RA Dorstyn L., Read S.H., Quinn L.M., Richardson H., Kumar S.;
RT "DECAY, a novel Drosophila caspase related to mammalian caspase-3 and
RT caspase-7.";
RL J. Biol. Chem. 274:30778-30783(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Dorstyn L., Read S.H., Kumar S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunco J., Pacleab J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celnikier S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003713; AAF55329.1; -.
DR EMBL; AF130469; AAD54071.2; -.
DR EMBL; AY089242; AAL89980.1; -.
DR HSP; P42574; IPAU.
DR MEROPS; C14.022; -.
DR FlyBase; FBgn0028381; decay.
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:0004208; F:caspase-3 activity; IDA.
DR GO; GO:0004207; F:effector caspase activity; NAS.
DR GO; GO:0006915; P:apoptosis; IMP.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 308 AA; 34911 MW; 686DA39060EC78C1 CRC64;

Query Match 2.4%; Score 10; DB 5; Length 308;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 KPXLFFFIQAC 287
Db 162 KPXLFFFIQAC 171

RESULT 23
Q918J3
ID Q918J3 PRELIMINARY; PRT; 476 AA.
AC Q918J3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-8.
GN CASP8
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
DR EMBL; AF273220; AAF79207.1; -.
DR HSP; Q15806; IQDU.

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RC STRAIN=Bristol N2;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "The C. elegans genome project: Contiguous nucleotide sequence of over
 RT two megabases from chromosome III.";
 RL Nature 0:0-0(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Taich A.;
 RL "The sequence of C. elegans cosmid T15B12.";
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; U14634; AAA21560.1; -;
 DR PIR; B88455; B88455.
 DR HSP; Q06486; ICKJ.
 DR WormPep; T15B12.2; CE01404.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR00719; Prot_kinase
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00069; pkinase; 2.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 370 AA; 42308 MW; A485A/DCC6FB7599 CRC64;

 Query Match 2.2%; Score 9; DB 5; Length 370;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 131 IGSFGFGDV 139
 Db 57 IGSFGFGDV 65

 RESULT 27
 Q812G4 PRELIMINARY; PRT; 481 AA.
 AC Q812G4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CASP8 and FADD-like apoptosis regulator.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC029223; AAH29223.1; -;
 DR GO; GO:0016323; F:apoptosis regulator activity; IEA.
 DR GO; GO:0030693; F:caspace activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR001309; ICE_p20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF01335; DED; 2.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR SMART; SM00115; CASC; 1.
 DR SMART; SM00031; DED; 2.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR PROSITE; PS0168; DED; 2.
 DR PROSITE; PS0168; DED; 2.
 SQ SEQUENCE 481 AA; 54874 MW; 433E07E2E5FA5A05 CRC64;

 Query Match 2.2%; Score 9; DB 11; Length 481;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 277 GKPKLFFIQ 285
 Db 352 GKPKLFFIQ 360

 RESULT 28
 Q942F3 PRELIMINARY; PRT; 1121 AA.
 AC Q942F3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative brassinosteroid-insensitive protein BRI1.
 GN P0480C01.13.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 RT clone: P0480C01.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AP003453; BAB68053.1; -;
 DR Gramene; Q942F3; -;
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007090; LRR_plant.
 DR InterPro; IPR00719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00560; LRR; 15.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 1121 AA; 120180 MW; F71A49B45E0E2D09 CRC64;

 Query Match 2.2%; Score 9; DB 10; Length 1121;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 131 IGSFGFGDV 139
 Db 813 IGSFGFGDV 821

 RESULT 29

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Q9LJF3
ID Q9LJF3 PRELIMINARY; PRT; 1164 AA.
AC Q9LJF3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Receptor protein kinase (AT3g13380/MRP15_1).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RV [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RL "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221 (2000).
RV [3]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones J., Kaniya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.W., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB000603; BAB01743.1; -.
DR EMBL; AY128280; AAM91089.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR plant.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00560; LRR; 15.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1164 AA; 126660 MW; 79380581D400EEC CRC64;

Query Match 2.2%; Score 9; DB 10; Length 1164;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 IGSGGFGDV 139
Db 864 IGSGGFGDV 872

RESULT 30
Q8LT85
ID Q8LT85 PRELIMINARY; PRT; 145 AA.
AC Q8LT85;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
OS Vibrio phage VpV262.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=194802;
RN [1]
RP SEQUENCE FROM N.A.
RA Hardies S.C.;
RT "The complete sequence of Vibriophage VpV 262.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY095314; AAM28362.1; -.
KW Hypothetical protein.
SQ SEQUENCE 145 AA; 16341 MW; 79B9720F88C1B998 CRC64;

Query Match 1.9%; Score 8; DB 9; Length 145;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 219 LARQDHGA 226
Db 14 LARQDHGA 21

RESULT 31
Q8H436
ID Q8H436 PRELIMINARY; PRT; 158 AA.
AC Q8H436;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE P0407H12.33 protein.
GN P0407H12.33.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
clone:P0407H12.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004303; BAC21455.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR001209; Ribosomal S14.
DR PROSITE; PS00527; RIBOSOMAL_S14; 1.
SQ SEQUENCE 158 AA; 17275 MW; AAD0FB7E5BA02983 CRC64;

Query Match 1.9%; Score 8; DB 10; Length 158;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LRRCLRL 16
Db 54 LRRCLRL 61

RESULT 32
Q970W7
ID Q970W7 PRELIMINARY; PRT; 165 AA.
AC Q970W7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

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DE Hypothetical protein ST1485.
GN ST1485.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshina T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
DR EMBL; AF000986; BAB66556.1; --
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 165 AA; 19200 MW; 4A39578B3CCA2400 CRC64;

Query Match 1.9%; Score 8; DB 17; Length 165;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 ALESRLGN 148
Db 99 ALESRLGN 106
|||||

RESULT 33
Q82TY7 PRELIMINARY; PRT; 266 AA.
ID Q82TY7
AC Q82TY7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DUF173.
GN NEI728.
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea.";
RL J. Bacteriol. 185:2759-2773(2003).
DR EMBL; BX321862; CAD85639.1; --
DR InterPro; IPR003768; DUF173.
DR Pfam; PF02616; DUF173; 1.
KW Complete proteome.
SQ SEQUENCE 266 AA; 30676 MW; 2E34DBA9452EA1DB CRC64;

Query Match 1.9%; Score 8; DB 16; Length 266;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 LALLELAR 221
Db 233 LALLELAR 240
|||||

RESULT 34
Q7V7P6 PRELIMINARY; PRT; 272 AA.
ID Q7V7P6
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```
AC Q7V7P6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABC transporter component, likely for sugar transport precursor.
GN PM00692.
OS Prochlorococcus marinus (strain MIT 9313).
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=74547;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642;
RA Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Stiglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX572097; CAE20867.1; --
KW Signal; Sugar transport; Complete proteome.
FT SIGNAL 1 36 Potential.
SQ SEQUENCE 272 AA; 30157 MW; 5FE29E9CA6855EA6 CRC64;
```

```
Query Match 1.9%; Score 8; DB 16; Length 272;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 214 LALLELAR 221
Db 117 LALLELAR 124
|||||
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RESULT 35
Q7U6Q4 PRELIMINARY; PRT; 272 AA.
ID Q7U6Q4;
AC Q7U6Q4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABC transporter, likely for trehalose/maltose, membrane component
DE precursor.
GN SYNW1284.
OS Synechococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=84588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825697; PubMed=12917641;
RA Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain P.,
RA Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I.,
RA Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synechococcus.";
RL Nature 424:1037-1042(2003).
DR EMBL; BX569692; CAE07799.1; --
KW Signal; Complete proteome.
FT SIGNAL 1 32 Potential.
SQ SEQUENCE 272 AA; 30051 MW; CODFDCFBA7B5D9E CRC64;
```

```
Query Match 1.9%; Score 8; DB 16; Length 272;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 214 LALLELAR 221
Db 117 LALLELAR 124
|||||
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```
RESULT 36
Q8YAX5 PRELIMINARY; PRT; 324 AA.
ID Q8YAX5
```

Q8YAX5;
 AC 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Oxidoreductase (EC 1.1.1.-).
 GN BMEI11126.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / Biotype 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mijer C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
 RA Jablonka L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyrpides N., Overbeek R.,
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 RL EMBL; AE009744; AAL54368.1; -.
 DR PIR; AE3650; AE3650.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000683; GFO_IDH_MCCA.
 DR Pfam; PF01408; GFO_IDH_MCCA; 1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 324 AA; 35683 MW; 3817F865ABDA4112 CRC64;
 Query Match 1.9%; Score 8; DB 16; Length 324;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 215 ALLELARQ 222
 Db 103 ALLELARQ 110
 Q9XAC4
 ID Q9XAC4 PRELIMINARY; PRT; 368 AA.
 AC Q9XAC4;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein SCO1932.
 GN SCO1932 OR SCO22.14C.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seeger K., Harris D.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapite D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajandream M.A., Rutterford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AJ939110; CAB50757.1; -.
 DR PIR; T36004; T36004.
 DR GO; GO:0004289; F:subtilase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000209; Peptidase S8.
 DR PROSITE; PS00136; SUBTILASE_ASP; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 368 AA; 38767 MW; DBF94549F6303FF0 CRC64;
 Query Match 1.9%; Score 8; DB 16; Length 368;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 EADRLRLR 10
 Db 81 EADRLRLR 88
 RESULT 38
 Q9KUW7
 ID Q9KUW7 PRELIMINARY; PRT; 372 AA.
 AC Q9KUW7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Aminotransferase, class V.
 GN VCO392.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae.";
 RL Nature 406:477-483(2000).
 DR EMBL; AE004127; AAF93565.1; -.
 DR PIR; G82328; G82328.
 DR TIGR; VC0392; -.
 DR GO; GO:0008483; F:transaminase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR000192; Aminotrans_V.
 DR Pfam; PF0266; aminotran_5; 1.
 DR PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
 KW Transferase; Complete proteome.
 SQ SEQUENCE 372 AA; 40623 MW; 00D5AFD1B6F6947B CRC64;
 Query Match 1.9%; Score 8; DB 16; Length 372;

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Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 GCPVSVEX 262
Db 119 GCPVSVEX 126
|||||

RESULT 39
Q8FXG8 PRELIMINARY; PRT; 378 AA.
AC Q8FXG8;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Oxidoreductase, Gfo/Idh/MocA family.
GN BRA0109.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Unayam L., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Krahl M., Shetty J., Malek J., Van Aken S.E.,
RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AS014514; AAN3319.1; -.
DR TIGR; BRA0109; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000683; GFO_IDH_MoCA.
DR Pfam; PF01408; GFO_IDH_MoCA; 1.
KW Complete proteome.
SQ SEQUENCE 378 AA; 41413 MW; 7F53CB86065F3787 CRC64;

Query Match 1.9%; Score 8; DB 16; Length 378;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 ALLELARQ 222
Db 103 ALLELARQ 110
|||||

RESULT 40
Q9IB63 PRELIMINARY; PRT; 399 AA.
AC Q9IB63;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Caspase-9.
GN XCASPASE-9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yaoita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family.";
RL J. Biol. Chem. 275:10484-10491(2000).

EMBL; AB038172; BAA94750.1; -.
DR HSP; Q15806; 1QDU.
DR MEROPS; C14.010; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR004488; Death.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCENZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS02029; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
SQ SEQUENCE 399 AA; 44772 MW; EE2A269719064F9F CRC64;

Query Match 1.9%; Score 8; DB 13; Length 399;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 LETRGSQA 69
Db 60 LETRGSQA 67
|||||

RESULT 41
Q801M6 PRELIMINARY; PRT; 415 AA.
AC Q801M6;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049286; AAH49286.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCENZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS02029; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hypothetical protein.

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OS *Xenopus laevis* (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI TaxID=8355;


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RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones." to the EMBL/GenBank/DBJ databases.
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
RA Toriumi M., Wallander E.K., Wong C., Wu H.C., Yamada K., Yu G.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis ORF clones." to the EMBL/GenBank/DBJ databases.
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC003974; AAC04493.1; -.
DR EMBL; AF367306; AAK32893.1; -.
DR EMBL; BT002219; AAN72230.1; -.
DR PIR; T00798; T00798.
DR InterPro; IPR006594; Lish.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINRPT.
DR SMART; SM00667; Lish; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS00896; LISH; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 3.
DR PROSITE; PS00882; WD_REPEATS_2; 5.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 787 AA; 85514 MW; 995B52584090CEC3 CRC64;

Query Match 1.9%; Score 8; DB 10; Length 787;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 FGDVGALE 143
Db 456 FGDVGALE 463
|||||

RESULT 48
O18107 PRELIMINARY; PRT; 794 AA.
AC O18107; 062283;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE H05L14.1 protein.
GN H05L14.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins J., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
RA Smaildon N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.; III of C.
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
```

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RL Nature 368:32-38 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RA McMurray A.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z99772; CAB16921.1; -.
DR EMBL; Z75550; CAB16921.1; JOINED.
DR EMBL; Z75550; CAA99932.1; -.
DR EMBL; Z99772; CAA99932.1; JOINED.
DR PIR; T23048; T23048.
DR HSSP; Q06486; ICKI.
DR WormPep; H05L14.1; CE16168.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00069; pkinase; 2.
DR ProDom; PD000001; Prot_kinase; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 2.
KW ATP-binding; Transferase.
SQ SEQUENCE 794 AA; 89743 MW; 8595E1971334DD5C CRC64;

Query Match 1.9%; Score 8; DB 5; Length 794;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 GSGGFGDV 139
Db 468 GSGGFGDV 475
|||||

RESULT 49
Q9VAX8 PRELIMINARY; PRT; 975 AA.
ID Q9VAX8
AC Q9VAX8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG4849 protein (LD28793p).
GN CG4849.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalusi F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=Berkeley;
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003763; AAF56769.1; -.
DR EMBL; AY089551; AAL90289.1; -.
DR FlyBase; FBgn0039566; CG4849.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
DR GO; GO:0006414; P:translational elongation; IEA.
DR InterPro; IPR000640; EFG.C.
DR InterPro; IPR009022; EFG-III.V.
DR InterPro; IPR005517; EFG-IV.
DR InterPro; IPR004161; EFTU D2.
DR InterPro; IPR000795; EF-GTPbind.
DR InterPro; IPR005225; Small GTP.
DR InterPro; IPR009000; Translat_factor.
DR Pfam; PF00679; EFG_C; 1.
DR Pfam; PF03764; EFG-IV; 1.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR PRINTS; PR00315; ELONGATNFCT.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
KW GTP-binding; Protein biosynthesis.
SQ SEQUENCE 975 AA; 110649 MW; 68A9072B3300E9CB CRC64;

Query Match 1.9%; Score 8; DB 5; Length 975;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 LLELARQD 223
Db 961 LLELARQD 968
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RESULT 50
Q962H8 PRELIMINARY; PRT; 1031 AA.
AC Q962H8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Membrane skeleton protein IMC2.
GN IMC2.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RH;
```

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RX MEDLINE=21313687; PubMed=11420112;
RA Mann T., Beckers C.;
RT "Characterization of the subpellicular network, a filamentous membrane
skeletal component in the parasite Toxoplasma gondii."
RL Mol. Biochem. Parasitol. 115:257-268(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RH;
RA Beckers C.J., Mann T.M.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY032682; AAK38356.2; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR004843; M-peptidase.
DR Pfam; PF00149; Metallophos; 1.
SQ SEQUENCE 1031 AA; 117427 MW; 9EAB3A0E148BE4F4 CRC64;

Query Match 1.9%; Score 8; DB 5; Length 1031;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 RAGSGSRR 52
Db 777 RAGSGSRR 784
|||||

Search completed: August 3, 2004, 09:10:45
Job time : 42 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 08:52:15 ; Search time 13 Seconds
(without alignments)
1666.245 Million cell updates/sec

Title: US-09-961-201a-1

Perfect score: 2180

Sequence: 1 MDEADRLRLRRCLRLVEEL.....YKQMPGCFNPLRKLFFKIS 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2166	99.4	416	1	ICE9 HUMAN
2	465	21.3	424	1	ICE2 CHICK
3	428	19.6	277	1	ICE3 CRIL0
4	418	19.2	277	1	ICE3 HUMAN
5	418	19.2	277	1	ICE3 MOUSE
6	411	18.9	435	1	ICE2 MOUSE
7	409	18.8	277	1	ICE3 RAT
8	409	18.8	435	1	ICE2 HUMAN
9	407	18.7	496	1	CE03 CAEUV
10	389.5	17.9	480	1	ICE8 MOUSE
11	387.5	17.8	503	1	CE03 CAEEL
12	383	17.6	479	1	ICE8 HUMAN
13	364.5	16.7	303	1	ICE7 MESAU
14	361.5	16.6	303	1	ICE7 HUMAN
15	350.5	16.1	303	1	ICE7 MOUSE
16	349	16.0	282	1	ICE3 XENLA
17	324	14.9	339	1	ICE DROME
18	322	14.8	276	1	ICE6 MOUSE
19	320	14.7	323	1	ICE1 DROME
20	312.5	14.3	312	1	ICE2 RAT
21	311.5	14.3	293	1	ICE6 HUMAN
22	305	14.0	521	1	ICEA HORSE
23	300.5	13.8	405	1	ICE1 SPOFR
24	297.5	13.6	299	1	ICEB XENLA
25	279	12.8	382	1	ICEB XENLA
26	278	12.8	404	1	ILBC PTG
27	274	12.6	410	1	ILBC FELCA
28	270.5	12.4	402	1	ILBC RAT
29	268.5	12.3	402	1	ILBC MOUSE
30	262	12.0	404	1	ILBC CANFA
31	259	11.9	404	1	ILBC HUMAN
32	256	11.7	386	1	ICEA XENLA
33	253	11.6	257	1	ICEE_MOUSE

34	239.5	11.0	242	1	ICEE HUMAN
35	232	10.6	377	1	ICED BOVIN
36	212	9.7	373	1	ICE4_MOUSE
37	210	9.6	418	1	ICE5_HUMAN
38	209	9.6	377	1	ICE4_HUMAN
39	207	9.5	419	1	ICEC_MOUSE
40	165	7.6	484	1	CFLA_MOUSE
41	147	6.7	480	1	CFLA_HUMAN
42	113.5	5.2	1612	1	RRPO_ORSVS
43	106.5	4.9	589	1	EGPI_MOUSE
44	98.5	4.5	915	1	SFB1_MOUSE
45	97.5	4.5	382	1	AMAC_HUMAN

ALIGNMENTS

RESULT 1
ICE9_HUMAN
ID ICE9_HUMAN STANDARD; PRT; 416 AA.
AC P55211; Q92852; Q9BQ62; Q9UEQ3; Q9UIJ8;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-9 precursor (EC 3.4.22.-) (CASP-9) (ICE-like apoptotic
DE protease 6) (ICE-LAP6) (Apoptotic protease Mch-6) (Apoptotic protease
DE activating factor 3) (APAF-3).
GN CASP9 OR MCH6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS VAL-28 AND ARG-221.
RA Duan H., Orth K., Chimariyan A.M., Poirier G.G., Froelich C.J.,
RA He W.-W., Dixit V.M.;
RT "ICE-LAP6, a novel member of the ICE/Ced-3 gene family, is activated
RT by the cytotoxic T cell protease granzyme B";
RL J. Biol. Chem. 271:16720-16724 (1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND PROCESSING.
RC TISSUE=T-cell;
RX MEDLINE=97059171; PubMed=8900201;
RA Srinivasula S.M., Fernandes-Alnemri T., Zangrilli J., Robertson M.,
RA Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,
RA Alnemri E.S.;
RT "The Ced-3/interleukin 1beta converting enzyme-like homolog Mch6 and
RT the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic
RT mediator CPP32";
RL J. Biol. Chem. 271:27099-27106 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99315341; PubMed=10384055;
RA Hadano S., Nasir J., Nichol K., Rasper D.M., Vaillancourt J.P.,
RA Sherer S.W., Beatty B.G., Ikeda J.E., Nicholson D.W., Hayden M.R.;
RT "Genomic organization of the human caspase-9 gene on chromosome
RT 1p36.1-p36.3";
RL Mamm. Genome 10:757-760 (1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=99168502; PubMed=10070954;
RA Srinivasula S.M., Almad M., Guo Y., Zhan Y., Lazebnik Y.,
RA Fernandes-Alnemri T., Alnemri E.S.;
RT "Identification of an endogenous dominant-negative short isoform of
RT caspase-9 that can regulate apoptosis";
RL Cancer Res. 59:999-1002 (1999).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Stomach cancer;
RA Izawa M., Mori T., Ito H., Sairenji T.;
RT "Molecular cloning and sequencing of a cDNA predicting an alternative
RT form of pro-caspase-9 from human gastric cancer cell lines";

Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
[6]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RP Miho Y., Momoi T., Fujita E.;
RA "A novel splicing product of human caspase-9 lacking protease
RT activity";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
[7]
RN SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANT VAL-28.
RX MEDLINE=99107856; PubMed=9890966;
RA Seol D.W., Billiar T.R.;
RT "A caspase-9 variant missing the catalytic site is an endogenous
RL inhibitor of apoptosis";
RL J. Biol. Chem. 274:2072-2076 (1999).
[8]
RN SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS VAL-28; LEU-99; ILE-102;
RP VAL-106; ASP-114; HIS-173 AND ARG-221.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RP Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
[9]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RA Thomas D.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
[10]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RT TISSUE=Eye, and Lymph;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Binding of caspase-9 to Apaf-
CC 1 leads to activation of the protease which then cleaves and
CC activates caspase-3. Proteolytically cleaves poly (ADP-ribose)
CC polymerase (PARP).
CC -!- FUNCTION: Isoform 2 lacks activity is an dominant-negative
CC inhibitor of caspase-9.
CC -!- SUBUNIT: Heterodimer of a 35 kDa (P35) and a 10 kDa (P10) subunit.
CC Caspase-9 and APAF1 bind to each other via their respective NH2-
CC terminal CED-3 homologous domains in the presence of cytochrome C
CC and ATP. Interacts with BIRC7.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=9L, Alpha;
CC IsoId=P55211-1; Sequence=Displayed;
CC Name=2; Synonyms=9S, Beta;
CC IsoId=P55211-2; Sequence=VSP_000818;
CC TISSUE SPECIFICITY: Ubiquitous, with highest expression in the
CC heart, moderate expression in liver, skeletal muscle, and
CC pancreas. Low levels in all other tissues.
CC -!- PTM: CLEAVAGES AT ASP-315 BY GRANZYME B AND AT ASP-330 BY CPP32
CC GENERATE THE TWO ACTIVE SUBUNITS. CASPASE-8 AND -10 CAN ALSO BE
CC INVOLVED IN THESE PROCESSING EVENTS.
CC -!- SIMILARITY: Belongs to peptidase family C14.

CC -!- SIMILARITY: Contains 1 CARD domain.
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EMBL; U56390; AAC50640.1; -;
EMBL; U60521; AAC50776.1; -;
EMBL; AB019205; BAA82697.1; -;
EMBL; AB019197; BAA82697.1; JOINED.
EMBL; AB019198; BAA82697.1; JOINED.
EMBL; AB019199; BAA82697.1; JOINED.
EMBL; AB019200; BAA82697.1; JOINED.
EMBL; AB019201; BAA82697.1; JOINED.
EMBL; AB019202; BAA82697.1; JOINED.
EMBL; AB019203; BAA82697.1; JOINED.
EMBL; AB019204; BAA82697.1; JOINED.
EMBL; AF093130; AAD12248.1; -;
EMBL; AB015653; BAA78780.1; -;
EMBL; AB020979; BAA87905.1; -;
EMBL; AF110376; AAD13615.1; -;
EMBL; AL512883; CAC42423.1; -;
EMBL; AY214168; AAO21133.1; -;
EMBL; BC002452; AAH02452.1; -;
EMBL; BC006463; AAH06463.1; -;
PDB; 3YGS; 19-APR-00.
MEROPS; C14.010; -;
Genew; HGNC:1511; CASP9.
MTM; 602234; -;
GO; GO:0004211; F:caspase-9 activity; TAS.
GO; GO:0004397; F:cysteine-type endopeptidase activity; TAS.
GO; GO:0008047; F:enzyme activator activity; TAS.
GO; GO:0008233; F:peptidase activity; TAS.
GO; GO:0008632; P:apoptotic program; TAS.
GO; GO:0008635; P:caspase activation via cytochrome c; TAS.
InterPro; IPR001315; CARD.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
InterPro; IPR002398; Peptidase_C14.
Pfam; PF00619; CARD; 1.
Pfam; PF00656; Peptidase_C14; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00114; CARD; 1.
SMART; SM00115; CARD; 1.
PROSITE; PS02029; CARD; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS02027; CASPASE_P10; 1.
PROSITE; PS02028; CASPASE_P20; 1.
Hydrolase; Thiol protease; Zymogen; Apoptosis; Alternative splicing;
KW Polymorphism; 3D-structure.
FT PROPEP 1 ?
FT CHAIN ? 315
FT PROPEP 316 330
FT CHAIN 331 416
FT DOMAIN 1 92
FT ACT SITE 237 237
FT ACT SITE 287 287
FT VARSPPLIC 140 289
FT VARIANT 28 28
FT VARIANT 99 99
FT VARIANT 102 102
FT VARIANT 106 106
FT VARIANT 114 114
FT VARIANT 114 114

POTENTIAL.
CASPASE-9 SUBUNIT P35.
CASPASE-9 SUBUNIT P10.
CARD.
BY SIMILARITY.
Missing (in isoform 2).
/FTId=VSP_000818.
A -> V.
/FTId=VAR_015415.
S -> L.
T -> I (in dbSNP:2308941).
/FTId=VAR_015417.
L -> V (in dbSNP:2308938).
/FTId=VAR_015418.
E -> D (in dbSNP:2020897).


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Db 340 ACLKGTAAWRNTRKGSWYIEALTTVFAEDSRDTHVADMLVKVNRQIKQREGY--RPG 394
RESULT 3
ICE3_CRILLO STANDARD; PRT; 277 AA.
AC Q60431;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
DE (SCA-1).
DE CASP3 OR CPP32.
GN Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OC NCBI_TaxID=10030;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96183185; PubMed=8605870;
RA Wang X., Zielinski N.G., Yang J., Sakai J., Brown M.S.,
RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by
RT CPP32 during apoptosis."
RL EMBO J. 15:1012-1020(1996).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
CC element binding proteins (SREBPs) between the basic helix-loop-
CC helix leucine zipper domain and the membrane attachment domain.
CC Cleaves and activates caspase-6, -7 and -9 (BY similarity).
CC -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: CLEAVAGE BY GRANTZYME B, CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family C14.
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DR EMBL; U27463; AB01511.1; -
DR HSRP; P42574; IPAU.
DR MERO; C14.003; -
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR Hydrolase; Thiol protease; Zymogen; Apoptosis.
KW PROPEP 1 9
FT PROPEP 10 28 BY SIMILARITY.
FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
FT ACT_SITE 121 121 BY SIMILARITY.
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FT ACT_SITE 163 163 BY SIMILARITY.
SQ SEQUENCE 277 AA; 31612 MW; 0BF3A4590A2828A3 CRC64;

Query Match 19.6%; Score 428; DB 1; Length 277;
Best Local Similarity 33.2%; Pred. No. 4.9e-29; Indels 42; Gaps 4;
Matches 91; Conservative 51; Mismatches 90;

QY 150 DLAYILSMPEPCGHCLIIINNVNFCRESGLTRTGSGNIDCEKLRFRFSLSHFVMEVKGDILTA 209
DB 34 DSYKMDYEMGVCIILNNKNPKHSTGMTPRSGTDVDAKLRFTWALKYEVNRKNDLTR 93
QY 210 KXNVLALLELARQDHGALDCCVVVILSHGQASHLOFPQAVYGTDCSPVSEKIVNIENG 269
DB 94 EEIVELMNKASKEDHSKRSFVCLVLSHGDE-----GVIFGTG-PIDLKLTYSYFRG 145
QY 270 TSCPSLGGKPKLFFIOACGGEQKHGFVASTSPEDSGNSPEPDATPQEGRLTFDQL 329
DB 146 DYCRSLGPKLFIILQACRGTELDGIEYDSTGTEDDMT----- 183
QY 330 DAISLSTPDSIDIEVSYSTFPFGVSWRDPKSGSVYVETLDDIFQWHAHSDLOQLLRVAN 389
DB 184 --CQKIPVEADFLYAYSTAPGYYSWRNPKDGSWFIQSLCSMLKYAHKLEFHMILTRVR 241
QY 390 AVSVK-----GIYKMPGCFNPLRKLFF 413
DB 242 KVATEFESFLDSTFHAKQIQCIVSMILTKELYF 275

RESULT 4
ICE3_HUMAN STANDARD; PRT; 277 AA.
ID ICE3_HUMAN STANDARD; PRT; 277 AA.
AC P42574; Q96AN1; Q96KP2;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
DE (SCA-1).
DE CASP3 OR CPP32.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A., AND VARIANT GLU-190.
RC TISSUE=T-cell;
RX MEDLINE=95074098; PubMed=7983002;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RT "CPP32, a novel human apoptotic protein with homology to
RT Caenorhabditis elegans cell death protein Ced-3 and mammalian
RT interleukin-1 beta-converting enzyme."
RL J. Biol. Chem. 269:30761-30764(1994).
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=95292347; PubMed=7774019;
RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
RA Beidler D.R., Poirier G.G., Salvessen G.S., Dixit V.M.;
RT "Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
RT protease that cleaves the death substrate poly(ADP-ribose)
RT polymerase."
RL Cell 81:801-809(1995).
RN [3]
SEQUENCE FROM N.A.
RA Vallette F.M., Oliver L.J.;
RT "Control of the activation of the procaspase-3 by a sequence located
RT at the N-terminus of the p17 subunit."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
SEQUENCE FROM N.A., AND VARIANT GLU-190.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
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[5] SEQUENCE FROM N.A., AND VARIANT GIJ-190.
 RP TISSUE=Lymph;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 29-46 AND 175-193, AND FUNCTION.
 RX MEDLINE=95319529; PubMed=7596430;
 RA Nicholson D.W., Ali A., Thornberry N.A., Vaillancourt J.P., Ding C.K.,
 RA Gallant M., Gareau Y., Griffin P.R., Labelle M., Lazebnik Y.A.,
 RA Munday N.A., Raju S.M., Smulson M.E., Yamin T.-T., Li V.L.,
 RA Miller D.K.;
 RT "Identification and inhibition of the ICE/CED-3 protease necessary
 RT for mammalian apoptosis."
 RL Nature 376:37-43(1995).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.
 RX MEDLINE=96266352; PubMed=8673606;
 RA Rotonda J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,
 RA Labelle M., Peterson E.P., Rasper D.M., Ruel R., Vaillancourt J.P.,
 RA Thornberry N.A., Becker J.W.;
 RT "The three-dimensional structure of apopain/CPP32, a key mediator of
 RT apoptosis."
 RL Nat. Struct. Biol. 3:619-625(1996).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.
 RX MEDLINE=97197830; PubMed=9045680;
 RA Mittl P.R.E., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,
 RA Priestle J.P., Tomaselli K.J., Gruetter M.G.;
 RT "Structure of recombinant human CPP32 in complex with the
 RT tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone."
 RL J. Biol. Chem. 272:6539-6547(1997).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=20283632; PubMed=10821855;
 RA Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,
 RA Kikly K., Winkler J.D., Sung C.-M., Deboick C., Richardson S.,
 RA Levy M.A., DeWolf W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,
 RA Ryan M.D., Hattiwanger R.C., Liang P.-H., Janson C.A., McDevitt P.J.,
 RA Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
 RA Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.;
 RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7
 RT inhibit apoptosis and maintain cell functionality."
 RL J. Biol. Chem. 275:16007-16014(2000).
 RN [10]
 RP PROCESSING.
 RX MEDLINE=96353838; PubMed=8755496;
 RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
 RA Litwack G., Alnemri E.S.;
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
 RT apoptotic cysteine protease containing two FADD-like domains."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
 RN [11]

CLEAVAGE OF HUNTINGTIN.
 RP MEDLINE=96331285; PubMed=8696339;
 RX Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,
 RA Graham R.K., Bromm M., Kazemi-Esfarjani P., Thornberry N.A.,
 RA Vaillancourt J.P., Hayden M.R.;
 RT "Cleavage of huntingtin by apopain, a proapoptotic cysteine protease,
 RT is modulated by the polyglutamine tract."
 RL Nat. Genet. 13:442-449(1996).
 CC -!- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. At the onset of apoptosis it
 CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
 CC 216-Asp-1-Gly-217 bond. Cleaves and activates sterol regulatory
 CC element binding proteins (SREBPs) between the basic helix-loop-
 CC helix leucine zipper domain and the membrane attachment domain.
 CC Cleaves and activates caspase-6, -7 and -9. Involved in the
 CC cleavage of huntingtin.
 CC -!- ENZYME REGULATION: Inhibited by isatin sulfonamides.
 CC -!- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Highly expressed in lung, spleen, heart, liver
 CC and kidney. Moderate levels in brain and skeletal muscle, and low
 CC in testis. Also found in many cell lines, highest expression in
 CC cells of the immune system.
 CC -!- PTM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10
 CC GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
 CC PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
 CC ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
 CC OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
 CC AND VICE VERSA.
 CC -!- SIMILARITY: Belongs to peptidase family C14.
 CC -----
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 CC -----
 DR EMBL; UI3737; AAA65015.1; -;
 DR EMBL; UI3738; AAB60355.1; -;
 DR EMBL; U26943; AAA74929.1; -;
 DR EMBL; AJ413269; CAC88866.1; -;
 DR EMBL; AY219866; AAO25654.1; -;
 DR EMBL; BC016926; AAH16926.1; -;
 DR PIR; A55315; A55315;
 DR PDB; 1PAU; 07-JUL-97.
 DR PDB; 1CF3; 24-DEC-97.
 DR PDB; 1GFW; 23-JUN-00.
 DR MEROPS; C14.003; -;
 DR Genew; HGNC:1504; CASP3.
 DR MIM; 600636; -;
 DR GO; GO:0004208; F:caspase-3 activity; TAS.
 DR GO; GO:0008624; P:induction of apoptosis by extracellular sig. .; TAS.
 DR GO; GO:0008629; P:induction of apoptosis by intracellular sig. .; TAS.
 DR GO; GO:0009403; P:pathogenesis; TAS.
 DR InterPro; IPR002138; ICE p10.
 DR InterPro; IPR001309; ICE p20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; ILIBCEZYME.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KW Hydrolase; Thiol protease; Zymogen; Apoptosis; Polymorphism;
 KW 3D-structure.
 FT PROPEP 1 9
 FT PROPEP 10 28
 FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
 FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
 FT ACT_SITE 121 121 BY SIMILARITY.

FT ACT_SITE 163 163 BY SIMILARITY.
 FT VARIANT 190 190 D -> E (in isoform beta).
 FT 31 36 /FTID=VAR_001401.
 FT 36 36 ISLDS -> MSWDG (IN REF. 3).
 FT STRAND 43 51
 FT STRAND 43 51
 FT HELIX 57 59
 FT TURN 60 60
 FT TURN 65 66
 FT HELIX 67 80
 FT TURN 81 82

Query Match 19.28; Score 418; DB 1; Length 277;
 Best local Similarity 33.24; Pred. No. 3.5e-28;
 Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAVLSMEPCGHLIINNUNFVRESGLRTRTSGNIDCEKLRFFSLHFMVEVKGDLTA 209
 Db 34 DSNKYMDYPEWGLCIILNNKFNHKSCTWTSRSGTDVDAANLRETFRLKYEVRKNLDR 93
 QY 210 KKMVLLLELARDHGDCCVVILSHGQASHLQFPGAVYGTGDCPVSVEKIVNIFNG 269
 Db 94 EEIVELMRDVKEDHSKRSFVCLLSHGEE-----GIPTGNG-PVDLKKITNFRG 145
 QY 270 TSCPSLGGKPLFIQACGGEQKHGPEVASTSPEDSPGSPNPEDATPPQGLRTDQL 329
 Db 146 DRCSLTGKPLFIQACRGTELDGLETGSDVDDM----- 182
 QY 330 DAISSLTPPSDIFVSYSFTFGFVSWRDPKSGSWYVETLDDIFEQWHSDEDLQSLLLRVAN 389
 Db 183 -ACHKIPVDADFLAYSTAPGYWRNSKDSWFIQSLCAMLKQYADKLEPMHILTVNR 241
 QY 390 AVSVK-----GIYKMPGCFNFKKLFF 413
 Db 242 KVATEFESFSDATFHAKQIPCIIVSLMTKELYF 275

RESULT 5
 ICE3 MOUSE STANDARD; PRT; 277 AA.
 AC P70677; Q08668; Q9QW14;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptain precursor (BC 3.4.22.-) (Cysteine protease CPP32) (Yama
 DE protein) (CPP-32) (Caspase-3) (SRBP cleavage activity 1)
 DE (SCA-1) (LICE).
 GN CASP3 OR CPP32.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96358624; PubMed=8761296;
 RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RA Fletcher F.A.;
 RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
 RT a cysteine protease resembling interleukin-1 beta converting enzyme
 RT and CED-3.";
 RL Oncogene 13:749-755(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224429; PubMed=9070890;
 RA Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.;
 RT "Specific expression of Cpp32 in sensory neurons of mouse embryos and
 RT activation of Cpp32 in the apoptosis induced by a withdrawal of
 RT NGF";
 RL Biochem. Biophys. Res. Commun. 231:770-774(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/An;
 RX MEDLINE=97190206; PubMed=9038361;

RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
 RA van Loo G., Molemans F., Schotte P., van Crielinge W., Beyaert R.,
 RT Fiers W.;
 RL "Characterization of seven murine caspase family members.";
 RN FEBS Lett. 403:61-69(1997).
 RP [4]
 RC SEQUENCE FROM N.A.
 RA TISSUE=Brain;
 RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA STRAIN=FVB/N; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Reingold E.A., Grouse L.H., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.F., Ruben G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smalusz D.B.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 58-277 FROM N.A.
 RA Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,
 RA Fortin J.-P., Sekaly R.-P.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. At the onset of apoptosis it
 CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
 CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
 CC element binding proteins (SRBPs) between the basic helix-loop-
 CC helix leucine zipper domain and the membrane attachment domain.
 CC Cleaves and activates caspase-6, -7 and -9 (By similarity).
 CC Cleaves Ii-1 beta between an Asp and an Ala, releasing the mature
 CC cytokine which is involved in a variety of inflammatory processes.
 CC -!- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
 CC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Highest expression in spleen, lung, liver,
 CC kidney and heart. Lower expression in brain, skeletal muscle and
 CC testis.
 CC -!- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -!- SIMILARITY: Belongs to peptidase family C14.
 CC
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 CC
 CC EMBL; U54803; AAC52768.1;
 CC EMBL; U54802; AAC52768.1; JOINED.
 DR
 DR

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DR EMBL; U49929; AAC52764.1; -.
DR EMBL; D86352; BAA21727.1; -.
DR EMBL; Y13086; CAA73528.1; -.
DR EMBL; U19522; AAC53196.1; -.
DR EMBL; BC038825; AAH38825.2; -.
DR EMBL; U63720; RAD09504.1; -.
DR PIR; JCS410; JCS410.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.003; -.
DR MGD; MGI:107739; Casp3.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; ILLBCEZYME.
DR PRINTS; PR00376; ILLBCEZYME.
DR SMART; SM00115; CASP; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 9
FT PROPEP 10 28 BY SIMILARITY.
FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
FT ACT_SITE 121 121 BY SIMILARITY.
FT ACT_SITE 163 163 BY SIMILARITY.
FT CONFLICT 17 17 E -> G (IN REF. 2).
FT CONFLICT 51 51 SRS -> ARN (IN REF. 6).
FT CONFLICT 63 65 SRS -> T (IN REF. 2).
FT CONFLICT 84 84 Q -> E (IN REF. 2).
FT CONFLICT 95 95 D -> E (IN REF. 2).
FT CONFLICT 97 97 L -> M (IN REF. 2).
FT CONFLICT 128 128 Y -> F (IN REF. 2).
FT CONFLICT 135 135 E -> D (IN REF. 2).
FT CONFLICT 231 231 E -> Q (IN REF. 6).
FT CONFLICT 262 262 I -> F (IN REF. 6).
SQ SEQUENCE 277 AA; 31474 MW; CE91598F74826605 CRC64;

Query Match 19.2%; Score 418; DB 1; Length 277;
Best Local Similarity 32.8%; Pred. No. 3.5e-28;
Matches 90; Conservative 50; Mismatches 92; Indels 42; Gaps 4;

QY 150 DLAYILSMPCGCHLIINNVNCRSGLTRGCSNIDCKELRRSSLLHFMVVEKGLTA 209
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
34 DSYKMDYFEMGICLIINNKHNHFKSGMSRSGTDVDAANLRETFMGLKYQYVRNKNLFR 93
QY 210 KKMVLALLELARQDHGALDCCVWVILSHGQASHLQFPGAVYGTDCPVSVEKIVNIENG 269
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
94 EDILELMDVSKEHDSKRSFVCLVILSHGDE-----GVYGTNG-FVELKKLTSFFRG 145
QY 270 TSCPSLGGKPKLFFTOACGEGEKDGHGFVASTSPEDSGSNPEPDATPFQGLRTFDQL 329
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
146 DYCRLTGKPKLFIQACRGTELDGCIETDSDGTEBEM----- 182
QY 330 DAISLPTPSDFVSYSFPPGVSRWDRPKSGWYVETLDDIEQWAHSEDLOSLLRVAN 389
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
183 -ACQIPVEADFLYAYSTAPGYISWRNSKOGSWFIOQLCSMLKLYAHKLEFHLITRVNR 241
QY 330 AVSVK-----GIYKMPGCFNFLRKKLFF 413
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
242 KVATEFESFLDSTFHAKKQIPCIVSMLTKELYF 275

RESULT 6
ICE2 MOUSE
ID ICE2 MOUSE STANDARD; PRT; 435 AA.
AC P29594; O08737;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEDD2 protein).

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GN OS CASP2 OR ICH1 OR NEDD2 OR NEDD-2.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=95047319; PubMed=7958843;
RA Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;
RT "Induction of apoptosis by the mouse Nedd2 gene, which encodes a
RT protein similar to the product of the Caenorhabditis elegans cell
RT death gene ced-3 and the mammalian IL-1 beta-converting enzyme.";
RL Genes Dev. 8:1613-1626(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
RA van Loo G., Molemans F., Schotte P., van Crielinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
RN [3]
RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92328780; PubMed=1378265;
RA Kumar S., Tomooka Y., Noda M.;
RT "Identification of a set of genes with developmentally down-regulated
RT expression in the mouse brain.";
RL Biochem. Biophys. Res. Commun. 185:1155-1161(1992).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Might function by either
CC activating some proteins required for cell death or inactivating
CC proteins necessary for cell survival. May be important in
CC multistep carcinogenesis.
CC -!- SUBUNIT: Heterodimer of a small and a large subunit (By
CC similarity).
CC -!- TISSUE SPECIFICITY: High level expression seen in the embryonic
CC CNS, liver, lung, kidney, small intestine, and hair follicles of
CC vibrissae. Moderate expression seen in the skin, oral mucosa,
CC skeletal muscle, submandibular gland and thymus. In the adult, it
CC is highly expressed in spleen, lung and kidney. Moderately in the
CC brain, heart, testis, liver. Low levels in the thymus, skeletal
CC muscle, ovary and gut.
CC -!- DEVELOPMENTAL STAGE: During embryonic development is highly
CC expressed in several types of mouse tissue undergoing high rates
CC of programmed cell death such as central nervous system and
CC kidney.
CC -!- PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC
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CC
CC EMBL; D28492; BAA25876.1; ALT_INIT.
CC EMBL; Y13085; CAA73527.1; ALT_INIT.
CC HSSP; P42574; 1CP3.
CC MEROPS; C14.006; -.
CC MGD; MGI:97295; Casp2.
CC InterPro; IPR001315; CARD.
CC InterPro; IPR002138; ICE_p10.
CC InterPro; IPR001309; ICE_p20.
CC InterPro; IPR002398; Peptidase_C14.
CC Pfam; PF00619; CARD; 1.
CC Pfam; PF00656; Peptidase_C14; 1.

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DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 9
FT PROPEP 10 28
FT CHAIN 29 175
FT CHAIN 176 277
FT ACT_SITE 121 121
FT ACT_SITE 163 163
FT CONFLICT 25 29
FT CONFLICT 170 170
FT CONFLICT 178 178
FT CONFLICT 182 182
FT CONFLICT 187 187
FT CONFLICT 190 190
FT CONFLICT 199 199
FT CONFLICT 211 211
FT CONFLICT 236 236
FT CONFLICT 245 245
SQ SEQUENCE 277 AA; 31491 MW; ADABF418E2507402 CRC64;

Query Match
Best Local Similarity 32.1%; Score 409; DB 1; Length 277;
Matches 88; Conservative 52; Mismatches 92; Indels 42; Gaps 4;

QY 150 DLAYILSMPCGCHLNNVNFRCESGLRTRTGSNIDCEKLRFRFSLHFMVVEKGLTA 209
Db 34 DSSYKMDYFEMGLCIINNNKFNHFKTGMARSARNTDVAANLRTFMALKYEVKNKDLTR 93

QY 210 KMWLVALLLEARDHGALDCCVVVILSHGCOASHLOFPAGVYGTDCGPVSVEKIVNFNG 269
Db 94 EEIMELMDSVSKEDHDKSRFSFVCIILSHGDE-----GVIFGTNG-PVDLKKLTFFFRG 145

QY 270 TSCPSLGGPKPLFFIOACGGEQKHGFVAVASTPEDESFGNSPEPPATPFQGLRFTDQL 329
Db 146 DYCRLITGPKPLFIIOACRGTELDGIEFTSGTDDM----- 182

QY 330 DAISLPTSDIFVSYSTFGFVSWDPKSGSVYVETLDDIFEQWAHSDLSLLLRVAN 389
Db 183 -ACQKIPVEADFLYAYSTAPGYYSWNSRDGWFQISLCAMLYAHKLEFHWHLTRVNR 241

QY 390 ANSVK-----GIYQMPCFNFLLKKLFF 413
Db 242 KVATEFESFSLDATHAKKQIIPCIVSMLTKELYF 275

RESULT 8
ICE2 HUMAN
ID ICE2 HUMAN STANDARD; PRT; 435 AA.
AC P42575; P42576;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1L/18).
DE CASP2 OR ICH1.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Buthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Fetal brain;
RX MEDLINE=94373811; PubMed=8087842;
RA Wang L., Miura M., Bergeron L., Zhu H., Yuan J.;
RT "Ich-1, an Ice/ced-3-related gene, encodes both positive and negative
RL regulators of programmed cell death.";
RL Cell 78:739-750(1994).
RN [2]
SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LEU-155; ALA-161 AND
RP GLY-424.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RP Doebber A., Martinka S., Maupin R.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RN CLEAVAGE SITES.
RX MEDLINE=96206041; PubMed=8654923;
RA Xue D., Shaham S., Horvitz H.R.;
RT "The Caenorhabditis elegans cell-death protein CED-3 is a cysteine
RT protease with substrate specificities similar to those of the human
RT CPP32 protease.";
RT Genes Dev. 10:1073-1083(1996).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Might function by either
CC activating some proteins required for cell death or inactivating
CC proteins necessary for cell survival.
CC -!- SUBUNIT: Heterodimer of a small and a large subunit (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS.
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Isoforms differ in the N- and C-termini;
CC Name=ICH-1L;
CC IsoId=P42575-1; Sequence=Displayed;
CC Name=ICH-1S;
CC Note=Acts as a positive regulator of apoptosis;
CC IsoId=P42575-2; Sequence=VSP_000801, VSP_000802;
CC Note=Acts as a negative regulator of apoptosis;
CC -!- TISSUE SPECIFICITY: Expressed in larger amounts in the embryonic
CC lung, liver and kidney than in the heart and brain. In the adults
CC higher level expression is seen in the placenta, lung, kidney,
CC pancreas than in the heart, brain, liver and skeletal muscle.
CC -!- PTM: THE MAJORITY PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES.
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -----
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CC -----
DR EMBL; U13021; AAA58959.1; -
DR EMBL; U13022; AAA58960.1; -
DR EMBL; AY219042; AAO25653.1; -
DR EMBL; AC073342; AAP22346.1; -
DR PIR; A54821; A54821.
DR HSP; P29466; IICB.
DR MEROPS; C14.006; -.
DR Genew; HGNC:1503; CASP2.
DR MIM; 600639; -.
DR GO; GO:0004202; F:caspase-2 activity; TAS.
DR GO; GO:0019893; F:enzyme binding; ISS.
DR GO; GO:0008633; F:apoptotic program; TAS.
DR GO; GO:0006508; F:proteolysis and peptidolysis; TAS.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001309; ICE p10.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS02029; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.

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DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolase; thiol protease; Apoptosis; Zymogen; Polymorphism;
FT PROPEP 1 152
FT CHAIN 153 308
FT PROPEP 309 316
FT CHAIN 317 435
FT CHAIN 331 435
FT CHAIN 15 103
FT DOMAIN 260 260
FT ACT SITE 303 303
FT ACT SITE 303 303
FT VARSPLIC 1 14
FT VARSPLIC 306 435
FT VARSPLIC 155 155
FT VARIANT 161 161
FT VARIANT 424 424
FT MUTAGEN 303 303
FT MUTAGEN 352 352
FT SEQUENCE 435 AA; 48855 MW; 1652EC73F6286FB7 CRC64;

Query Match
Best Local Similarity 29.5%; Pred. No. 3.8e-27; Length 435;
Matches 127; Conservative 66; Mismatches 155; Indels 82; Gaps 13;

Qy 9 LRRCLRLVLEQVDLQWLVLLSRELFPHMIEDIQ-RAGSGRRDQARQLIIDEITRGS 67
Db 23 LKNKRVVLAKQLLSLELLEHLEKDIITLENRELIQAKVGSFS---QNVELLNLLPKRP 79
Qy 68 QALPLFTSLCDETDQDMLASFLRN-----
Db 80 QAFDAFCALRETKQGHLEDMLLTSLGLQHVLPPLSCDYDLSLPPFCVSCPLYKKLRL 139
Qy 99 SKPTLENLT-----PVVLRPEIRKPEVLRPTPRPDIGSGGFGDVGSALELRGNADLAY 153
Db 140 STDIVHSLDNKDGPVCLQ-----VKPCTP-----EFYQTHFQLAY 175
Qy 154 ILSMEPCGHCUIINNVNFCRSGRLRTGNSIDCEKLRRRFSLLHFMVEVKGDLTAKQW 213
Db 176 RLQSRPRGLALVLSNVHFTGTEKELEFRSGGVDHSTLVTLPKLLGYDVHVLCDQTAQEMQ 235
Qy 214 LALLELAR-QDHGALDCCVVVILSHGCOASHLQFPQVAVYGTGDCPVSVKEIVNIFNGTSC 272
Db 236 EKLQNFALPARRVTVDSICVALLSHGVE-----GALYGVDKLLQJQEVFQFQFDMANC 288
Qy 273 PSLGGKPKLFFIQACGGQKDHGEVASTSPEDSPGNSNPDPATPPQEGRLTFDQLDAI 332
Db 289 PSLQNKPKMFIQACRGDETRGVDDQDQKHNAGSPGCE-ESDA-----GREKLPKM--- 339
Qy 333 SSLTPSPDIFVSYSTFPQFVSWRDPKSGSWVETLDDIFEQWHAHSEDLOSLLLRVANAVS 392
Db 340 -RLPTRSDMIGCYACLKGTAAAMRNTRKGSWYIEALAQVFSERACDMHVDMLVKV-NAL- 396
Qy 393 VKGIYKQMPG 402
Db 397 IKDREGYAPG 406

RESULT 9
ID CED3 CAEUV STANDARD; PRT; 496 AA.
AC P45436;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)
Cell death protein 3 precursor (EC 3.4.22.-).
CED-3.
Caenorhabditis vulgariis.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=31233;
[1]
SEQUENCE FROM N.A.
MEDLINE=94061982; PubMed=8242740;
Yuan J., Shaham S., Ledoux S., Ellis H.M., Horvitz H.R.;
"The C. elegans cell death gene ced-3 encodes a protein similar to
mammalian interleukin-1 beta-converting enzyme.";
Cell 75:641-652(1993).
CC -!- FUNCTION: Acts as a cysteine protease in controlling programmed
cell death by proteolytically activating or inactivating a
substrate protein or proteins, a potential substrate may be ced-4.
Alternatively it might directly cause cell death by
proteolytically cleaving proteins that are crucial for cell
viability (By similarity).
CC -!- SUBUNIT: Could be a heterodimer of two subunits derived from the
precursor sequence by a probable autocatalytic mechanism.
CC -!- PTM: May be regulated by phosphorylation.
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -!- SIMILARITY: Contains 1 CARD domain.
DR HGSP; P42574; 1CP3.
DR MEROPS; C14.002; -.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis; Phosphorylation.
FT CHAIN 1 364
FT CELL DEATH PROTEIN 3 SUBUNIT 1
FT (POTENTIAL).
FT CELL DEATH PROTEIN 3 SUBUNIT 2
FT (POTENTIAL).
FT CHAIN 365 496
FT DOMAIN 1 91
FT ACT SITE 308 308
FT ACT SITE 351 351
FT ACT SITE 351 351
FT SEQUENCE 496 AA; 55945 MW; 58E73C790DC3BD38 CRC64;

Query Match
Best Local Similarity 18.7%; Score 407; DB 1; Length 496;
Matches 131; Conservative 74; Mismatches 159; Indels 170; Gaps 15;

Qy 1 MDEADRR-LLRRCRLRVLEQVDLQWLVLLSRELFPHMIEDIQRAGSG-----SRR 52
Db 1 MWRQDRRLLENILVFNKILQSEQLIDVLIK-----DVLSNDGDMINSCTER 51
Qy 53 DQARQLIIDLTRGSQALPLFISCLDTPGQDMLASFLR-----TNROAGKLS 99
Db 52 DKRKEQKAVQVRGDEAFDFRYDALRDTGHELLAAVLEPLATDLGCPSPASHRSRALS 111
Qy 100 KPTLENLTPVVL-----RPEIRKPEVLRPET 125
Db 112 PTFSSPFRVHRDSSVSSVSTSTVQDVVYTRASTSRSSRLPHTSDRHNYSVSPNSRPSQ 171
Qy 126 PRPVDIGSGFGDVGCALES-----LRGNADLAYILSM----- 158
Db 172 PSSANGSFTGCSLGYSSSRSTRSYSKASAHSCYIFHEEDMNYVDAPTHRVDEKTYRN 231
Qy 159 ---PCGHCLINNVNFCRESGLRTRTGSNIDCEKLRRRFSLLHFMVEVKGDLTAKKMLA 215
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Db 232 FSTPRGLCLINNEHF---EQMPTRNGTKADKONLWIFRCMGVTVICKONISGRGM-LT 287
Qy 216 LLELAROD-HGALDCCVVWILSHGQCASHIQFPGAVGTGDCPPVSVKIVNIFNGTSCPS 274
Db 288 IRDFARNETHG--DSAILVILSHGEE-----NVILGVDDVSVNVHIVDLLNAANAPR 338
Qy 275 LGGPKLFFTOACGGEOKHGFEVASVSPEDSPGSPNPDATPFQGLRFTFDOLDIAISS 334
Db 339 LANKPKLVFVQACGERDNGFPV-----LDSVDGVPS 371
Qy 335 L-----PTPSDFVSYSTFPFGVSWRDPKSGSWVET 366
Db 372 LIRRGWDRDGNFLGCVRPQAOQVWKKPSQADILIRYATTAGYVSWRNSARGSWFIQA 431
Qy 367 LDDIFQWHSBLSQILLRVANAVSV-----KGIYKQMGPCFNFLRKLJFF 413
Db 432 VCEVFSTHAKMDVDVVELLTVNKKVACGFGTSGANILKQMPBMTSLLLKKFYF 485

RESULT 10
IC38_MOUSE
ID IC38_MOUSE STANDARD; PRT; 480 AA.
AC 089110; O35669;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-8 precursor (BC 3.4.22.-).
GN CASP8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=129/SVJ;
RX MEDLINE=98316661; PubMed=9654089;
RA Sakamaki K., Teukumo S.-I., Yonehara S.;
RT "Molecular cloning and characterization of mouse caspase-8.";
RL Eur. J. Biochem. 253:399-405(1998).
RN [2]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=FVB/N; TISSUE=Colon, and Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
SEQUENCE OF 57-476 FROM N.A.
RP

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RA Kioschis P., Kischkel F., Poustka A., Kramer P.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Most upstream protease of the activation cascade of
CC caspases responsible for the TNFRSF6/FAS mediated and TNFRSF1A
CC induced cell death. Binding to the adapter molecule FADD recruits
CC it to either receptor. The resulting aggregate called death-
CC inducing signaling complex (DISC) performs CASP8 proteolytic
CC activation. The active dimeric enzyme is then liberated from the
CC DISC and free to activate downstream apoptotic proteases.
CC Proteolytic fragments of the N-terminal propeptide (termed CAP3,
CC CAP5 and CAP6) are likely retained in the DISC. Cleaves and
CC activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
CC participate in the G2M6 apoptotic pathways. Cleaves ADPRT.
CC Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC.
CC Likely target for the cowpox virus CPWA death inhibitory protein.
CC -!- ENZYME REGULATION: Inhibited by Z-VAD-FK, Crma and P35.
CC -!- SUBUNIT: Heterodimer of a 18 kDa (P18) and a 10 kDa (P10) subunit.
CC Interacts with Fadd, Cflar and Peals (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in a wide variety of tissues.
CC Highest expression in spleen, thymus, lung, liver and kidney.
CC Lower expression in heart, brain, testis and skeletal muscle.
CC -!- DEVELOPMENTAL STAGE: In the embryo, highest expression occurs at
CC day 7.
CC -!- PIM: Generation of the subunits requires association with the
CC death-inducing signaling complex (DISC), whereas additional
CC processing is likely due to the autocatalytic activity of the
CC activated protease. GZMB and CASP10 can be involved in these
CC processing events (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -!- SIMILARITY: Contains 2 death effector (DED) domains.
CC -----
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CC -----
DR EMBL; AF067841; AAC40132.1; -
DR EMBL; AF067835; AAC40132.1; JOINED.
DR EMBL; AF067836; AAC40132.1; JOINED.
DR EMBL; AF067837; AAC40132.1; JOINED.
DR EMBL; AF067838; AAC40132.1; JOINED.
DR EMBL; AF067839; AAC40132.1; JOINED.
DR EMBL; AF067840; AAC40132.1; JOINED.
DR EMBL; AF067834; AAC40131.1; -
DR EMBL; AF067834; AAC40131.1; -
DR EMBL; AJ007749; CAA07677.1; -
DR EMBL; BC006737; AAH06737.1; -
DR EMBL; BC049955; AAH49955.1; -
DR EMBL; AJ000641; CAA04196.1; -
DR HSSP; Q15806; 1QDU.
DR MEROPS; C14.009; -
DR MGD; MGI:1261423; Casp8.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0004205; F:caspase-8 activity; IDA.
DR GO; GO:0006915; P:apoptosis; IDA.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYME.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CVS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_F20; 1.
DR PROSITE; PS0168; DED; 2.
KW Hydrolase; Thiol protease; Apoptosis; Zymogen; Repeat.

```



```
Query Match      17.8%; Score 387.5; DB 1; Length 503;
Best Local Similarity 25.0%; Pred. No. 3.2e-25;
Matches 128; Conservative 79; Mismatches 188; Indels 117; Gaps 17;

QY 1 MDEADDR-LLRRCLRRLVEELQVDQLMDVLLSLRFLPHMEDIQRAGSGRRDQARQLI 59
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MMQRDSLLRLNRTMFSHLKVDIEILVIAKOVLSNDGMDIN--SCGTVRKRREIV 58
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 IDLETRGQALPIFISCLEDTGQDMLASFIR-----TTRQAGKLS 99
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 KAVQRRGDVAFDAFYDALRSTGHEGLAEVLEPLARSVDNSNAVEPCPMPASHRRSRLS 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 100 -----KPT-----LENLTPVLRPERK-----PEVLRPETP 126
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 PAGYTSRVRHDSVSVSFTSYQDIYSRARSRSRALHSDRHNYSSPPVNAFPSP 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 127 RPVDIGSGGFGDVGALES-----LRGNADLAYILSMB----- 158
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 179 SSANSFTGCGSSLYSSRRNSFSKASGPTQYIFHEEDMMFVDAPTTSRVFDEKTMVRF 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 159 --PCGHCLINNNFCKESGLRTRTGSNIDCEKLRFRFSLHFVVEVKGDLTAKKMWIAL 216
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 239 SSPRGMLIINNEHF---EQMPTRNGTKADKDNLTNLCRCMGYTVICKDNLTGRGMLITI 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 217 LELAR-QDHGALCCVVVILSHGQASHLQFPAGVYGTDCPVSVEKIVNIFNGTSCPSL 275
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 296 RDFAKHESHG--DSAILVILSHGEE-----NVIIGVDDIPITSTHEIYDLLMAANAPRL 346
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 276 GGRPKLFFIIQACGGEQKDHGFVASTSPEDESPQ-----SNPEPATPFOEGLRTFDOL 329
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 347 ANKPKLVFVQACGRERDNGFPVLDS--VGVPAFLRRGWDRDGLPFLNGCVR--PQV 402
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 330 DAI--SSLPTSDIFVSYSTFPFGVWNRDPKSGSWYVETLDDIFEQWAHSEDLQSLLRVA 388
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 403 QQVWRKKPSQADILLIAYATTAQVSVWRNSARGSWFIQAVCEVFTSHAKMDVVVELLTVN 462
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 389 NAVSV-----KGIVKQMPGCCNFLEKKLFF 413
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 463 KKVACGFQTSQGSNLIKQMPMTSRLKKFYF 494
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
ICE8 HUMAN
ID ICE8_HUMAN STANDARD; PRT; 479 AA.
AC Q14790; Q14676; Q14791; Q14792; Q14793; Q14794; Q14795; Q14796;
AC Q15780; Q15806; Q8TD11; Q8TD12; Q8TD13; Q8TD14; Q8TD15; Q96T22;
AC Q9COK4; Q9UQ01;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase-8 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 5)
DE (MORT1-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-
DE like protease) (FADD-like ICE) (FLICE) (Apoptotic cysteine protease)
DE (Apoptotic protease Mch-5) (CAP4).
GN CASP8 OR MCH5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 5; 6; 7 AND 8).
RC TISSUE=B-cell, and Thymus;
RX MEDLINE=96279826; PubMed=8681376;
RA Boldin M.P., Goncharov T.M., Goltsev Y.V., Wallach D.;
RT "Involvement of MACH, a novel MORT1/FADD-interacting protease, in
RT Fas/APO-1- and TNF receptor-induced cell death.";
RL Cell 85:803-815(1996).
RN [2]
SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
RX MEDLINE=96279827; PubMed=8681377;
RA Muzio M., Chinnaiyan A.M., Kischkel F.C., O'Rourke K., Shevchenko A.,
RA Ni J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann M.,
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RA Krammer P.H., Peter M.B., Dixit V.M.;
RT "FLICE, a novel FADD-homologous ICE/CED-3-like protease, is recruited
RT to the CD95 (Fas/APO-1) death-inducing signaling complex.";
RL Cell 85:817-827(1996).
RN [3]
SEQUENCE FROM N.A. (ISOFORM 4).
RC TISSUE=T-cell;
RX MEDLINE=96353838; PubMed=8755496;
RA Fernandes-Alnemri T., Armstrong R.C., Krebs J.F., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemri E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FADD-like domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
RN [4]
SEQUENCE FROM N.A.
RX MEDLINE=99132295; PubMed=9931493;
RA Grenet J., Teitz T., Wei T., Valentine V., Kidd V.J.;
RT "Structure and chromosome localization of the human CASP8 gene.";
RL Gene 226:225-232(1999).
RN [5]
SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=97373543; PubMed=9228018;
RA Srinivasula S.M., Ahmad M., Ottilie S., Bullrich F., Banks S.,
RA Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
RA Armstrong R.C., Alnemri E.S.;
RT "FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates
RT Fas/TNFR1-induced apoptosis.";
RL J. Biol. Chem. 272:18542-18545(1997).
RN [6]
SEQUENCE FROM N.A.
RX MEDLINE=21100893; PubMed=11161814;
RA Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
RA Ikeda J.-E., Hayden M.R.;
RT "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
RT and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
RT critical region at chromosome 2q33-q34: candidate genes for ALS2.";
RL Genomics 71:200-213(2001).
RN [7]
SEQUENCE FROM N.A. (ISOFORM 7), AND FUNCTION OF ISOFORM 7.
RC TISSUE=Leukocyte;
RX MEDLINE=22005982; PubMed=12010809;
RA Himeji D., Horiuchi T., Tsukamoto H., Hayashi K., Watanabe T.,
RA Harada M.;
RT "Characterization of caspase-8L: a novel isoform of caspase-8 that
RT behaves as an inhibitor of the caspase cascade.";
RL Blood 99:4070-4078(2002).
RN [8]
SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 9), AND INTERACTION OF ISOFORM 9
RP WITH BCAP31 AT THE ENDOPLASMIC RETICULUM.
RX MEDLINE=21927603; PubMed=11917123;
RA Breckenridge D.G., Nguyen M., Kuppig S., Reth M., Shore G.C.;
RT "The procaspase-8 isoform, procaspase-8l, recruited to the BAP31
RT complex at the endoplasmic reticulum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336(2002).
RN [9]
SEQUENCE FROM N.A. (ISOFORM 7).
RC TISSUE=Leukocyte;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hellon E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Kryzyski M.I., Skalska U., Smalus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [10]
RP PARTIAL SEQUENCE, AND PROCESSING.
RX MEDLINE=97121412; PubMed=962078;
RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
RA Alnemri E.S.;
RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
RT protease Mch5 is a CrmA-inhibitable protease that activates multiple
RT Ced-3-like cysteine proteases.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491 (1996).
RN [11]
RP FUNCTION.
RX MEDLINE=97160607; PubMed=9006941;
RA Muzio M., Salvesen G.S., Dixit V.M.;
RT "FICE induced apoptosis in a cell-free system. Cleavage of caspase
RT zymogens.";
RL J. Biol. Chem. 272:2952-2956 (1997).
RN [12]
RP PROCESSING.
RX MEDLINE=97327557; PubMed=9184224;
RA Medema J.P., Scaffidi C., Kischkel P.C., Shevchenko A., Mann M.,
RA Krammer P.H., Peter M.E.;
RT "FICE is activated by association with the CD95 death-inducing
RT signaling complex (DISC).";
RL EMBO J. 16:2794-2804 (1997).
RN [13]
RP CHARACTERIZATION OF ISOFORM 7.
RX MEDLINE=20318377; PubMed=10860845;
RA Horiuchi T., Himeji D., Tsukamoto H., Harashima S., Hashimura C.,
RA Hayashi K.;
RT "Dominant expression of a novel splice variant of caspase-8 in human
RT peripheral blood lymphocytes.";
RL Biochem. Biophys. Res. Commun. 272:877-881 (2000).
RN [14]
RP INTERACTION WITH BCL2; BCL2L1 AND BCAP31.
RX MEDLINE=97477382; PubMed=9334338;
RA Ng F.W.H., Nguyen M., Kwan T., Branton P.E., Nicholson D.W.,
RA Cromlish J.A., Shore G.C.;
RT "p28 Bap31, a Bcl-2/Bcl-XL- and procaspase-8-associated protein in the
RT endoplasmic reticulum.";
RL J. Cell Biol. 139:327-338 (1997).
RN [15]
RP INTERACTION WITH PEAL5.
RX MEDLINE=99369240; PubMed=1042631;
RA Condorelli G., Vigliotta G., Cafieri A., Trencia A., Andalo P.,
RA Oriente F., Miele C., Caruso M., Formisano P., Beguinot F.;
RT "PED/PEA-15: an anti-apoptotic molecule that regulates Fas/TNFR1-
RT induced apoptosis.";
RL Oncogene 18:4409-4415 (1999).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=99451259; PubMed=10508784;
RA Blanchard H., Kodandapani L., Mittl P.R.E., Di Marco S., Krebs J.F.,
RA Wu J.C., Tomaselli K.J., Gruetter M.G.;
RT "The three-dimensional structure of caspase-8: an initiator enzyme in
RT apoptosis.";
RL Structure 7:1125-1133 (1999).
RN [17]
RP VARIANT CASP8 TRP-248.
RX MEDLINE=22239940; PubMed=12353035;
RA Chun H.J., Zheng L., Ahmad M., Wang J., Speirs C.K., Siegel R.M.,
RA Dale J.K., Puck J., Davis J., Hall C.G., Skoda-Smith S.,
RA Atkinson T.P., Straus S.E., Lenardo M.J.;
RT "Pleiotropic defects in lymphocyte activation caused by caspase-8
RT mutations lead to human immunodeficiency.";
RL Nature 419:395-399 (2002).
CC -!- FUNCTION: Most upstream protease of the activation cascade of

CC caspases responsible for the TNFRSF6/FAS mediated and TNFRSF1A
CC induced cell death. Binding to the adapter molecule FADD recruits
CC it to either receptor. The resulting aggregate called death-
CC inducing signaling complex (DISC) performs CASP8 proteolytic
CC activation. The active dimeric enzyme is then liberated from the
CC DISC and free to activate downstream apoptotic proteases.
CC Proteolytic fragments of the N-terminal propeptide (termed CAP3,
CC CAP5 and CAP6) are likely retained in the DISC. Cleaves and
CC activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
CC participate in the G2M6 apoptotic pathways. Cleaves ADPRT.
CC Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC.
CC Likely target for the coxox virus CRMA death inhibitory protein.
CC Isoforms 5, 6, 7 and 8 lack the catalytic site and may interfere
CC with the pro-apoptotic activity of the complex.
CC -!- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 10 kDa (p10) subunit.
CC Interacts with FADD, CFLAR and PEAL5. Isoform 9 interacts at the
CC endoplasmic reticulum with a complex containing BCAP31, BAF29,
CC BCL2 and/or BCL2L1.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=9;
CC Name=1; Synonyms=Alpha-1;
CC IsoId=Q14790-1; Sequence=Displayed;
CC Name=2; Synonyms=Alpha-2, MCH5-beta;
CC IsoId=Q14790-2; Sequence=VSP_000810;

Query Match 17.6%; Score 383; DB 1; Length 479;
Best Local Similarity 25.2%; Pred. No. 7.2e-25;
Matches 122; Conservative 79; Mismatches 150; Indels 134; Gaps 17;
QY 5 DRLRLRRLRLVEELQVDQLVDVLSRELPRPHMIEDIQAGSGRRDQARQLIIDET 64
DB 50 EKMLESNLSFLKEL-----LFRINRL-DLLITYLNTKEEMER---ELQT 92
QY 65 RGSQALPLFTSCLEDQDMLASFLPNR--QAQKLSKPTLE---NLTPVVLREIR--- 116
DB 93 PGRAQISAYRVMYQISEVSRSELSRSLFKLLQEEISKCKLDDMNLDDIFIEKRVIL 152
QY 117 ---KPEVLR-----SESTLQDKVQMKSPRGYCLIIINHNFAKAREKVPKLSIRD 259
DB 180 RTGSNIDCEKLRPFSSLHFMVVKGDLTAKM--VLALLRLARQDHGALCCVVVILSH 237
DB 260 RNGTHLDAGALTTFEELHFEIKPHDDCTVEQIYEILKIYQI--MDHNSMDCFCICILSH 317
QY 238 GCQASHLQFPGAVYTGDCPVSVVEKIVNIFNGTSCPSLGGPKPLFFIACGGEQKDHGFE 297
DB 318 GDK-----GIIVGTGQEQAPIVELTSQFTGLKCPSLAGPKVFFIACQGDNYQKGP 370
QY 298 VASTSPEDSPGSPNPEPDATPFQGLRTFDQDLAISS-----LPTPSDIFVSVYPPGVS 353
DB 371 VETDSEEQ-----PYLE-----MDLSSPQTRYPIDAEFLGGMATVNNCVS 411
QY 354 WRDPKSGSWYVETL-DDIFEQWAHSEDLQSLI-----LEVANAVSVKGYKMGPCFNLR 408
DB 412 YRNFAEGWYIQSLCQSLRERCPRGDDILITLITVEVNEVSKDKKKNMGKMPQPTFTLR 471
QY 409 KKLFF 413
DB 472 KKLVF 476

RESULT 13
ICE7 MESAU
ID ICE7 MESAU STANDARD; PRT; 303 AA.
AC P55214;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

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OM protein - protein search, using sw model

Run on: August 3, 2004, 08:52:20 ; Search time 17 Seconds
(without alignments)
2353.863 Million cell updates/sec

Title: US-09-961-201a-1

Perfect score: 2180

Sequence: 1 MDEADRLRLRCRLRLVSL.....YKQMPCCFNLRKLLFFKTS 416

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2180	100.0	416	2 G02635	ICE-LAP6 - human
2	1658	76.1	454	2 JC7123	caspase-9 long cha
3	429	19.7	277	2 S64710	cysteine proteinas
4	418	19.2	277	2 A55315	cysteine proteinas
5	414	19.0	452	2 JC6507	caspase-2 - rat
6	409	18.8	435	2 A54821	apoptosis regulato
7	408	18.7	277	2 JC5410	CPP32 protein - mo
8	387.5	17.8	503	2 A49429	interleukin-1 beta
9	384	17.6	212	2 I67437	cysteine proteinas
10	362	16.6	495	2 T20038	hypothetical prote
11	304	13.9	312	2 B54821	apoptosis regulato
12	268.5	12.3	402	2 A64495	IL-1 beta converta
13	262	12.0	182	2 I67436	interleukin-1-beta
14	262	12.0	826	2 T43638	caspase-related pr
15	259	11.9	404	2 A42677	interleukin-1 beta
16	256.5	11.8	383	2 A56084	interleukin-1-beta
17	242.5	11.1	536	2 T43633	caspase-related pr
18	239.5	11.0	242	2 JC7517	caspase-14/a - hum
19	236	10.8	642	2 T27021	hypothetical prote
20	220	10.1	311	2 B56084	interleukin-1-beta
21	210	9.6	418	2 B57511	interleukin-1 beta
22	209	9.6	377	2 A57511	interleukin-1-beta
23	209	9.6	488	2 T13385	hypothetical prote
24	186	8.5	263	2 C56084	interleukin-1-beta
25	154.5	7.1	149	2 T43637	caspase protein 1C
26	151.5	6.9	136	2 I53300	interleukin-1-beta
27	115.5	5.3	394	2 T26968	hypothetical prote
28	108.5	5.0	589	2 T52070	RNA1 protein homol
29	107.5	4.9	139	2 T43642	caspase protein 3

RNA1 homolog fugu1
hypothetical prote
3-dehydroquinat d
polycystic kidney
microtubule-associ
alcohol dehydrogen
hypothetical prote
probable polygalac
hypothetical prote
hypothetical prote
Rbp9p related prot
testis-abundant fi
protein T2205.17 [
fibulin-2 precursor
proline-rich pepti
glucosyl transfera

ALIGNMENTS

RESULT 1

G02635

ICE-LAP6 - human

C/Species: Homo sapiens (man)

C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999

C/Accession: G02635

R/Duan, H.; Orth, K.; Chinnaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.; Dixit,

submitted to the EMBL Data Library, April 1996

A/Reference number: H01513

A/Accession: G02635

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-416 <DUA>

A/Cross-references: EMBL:U56390; NID:gl1336026; PIDN:AAC50640.1; PID:gl1336027

Query Match

Best Local Similarity 100.0%; Score 2180; DB 2; Length 416;

Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDEADRLRLRCRLRLVSLV	589	2	A36983
Db	1	MDEADRLRLRCRLRLVSLV	589	2	A36983
QY	61	DLETGSQLPLFISCLDTGD	589	2	A36983
Db	61	DLETGSQLPLFISCLDTGD	589	2	A36983
QY	121	LRPETPRPVDIGSGGFGD	589	2	A36983
Db	121	LRPETPRPVDIGSGGFGD	589	2	A36983
QY	181	TGSNIDCEKLRFRFSLH	589	2	A36983
Db	181	TGSNIDCEKLRFRFSLH	589	2	A36983
QY	241	ASHLOFPGAVYTDGCPV	589	2	A36983
Db	241	ASHLOFPGAVYTDGCPV	589	2	A36983
QY	301	TSPEDESGSNPEPDATP	589	2	A36983
Db	301	TSPEDESGSNPEPDATP	589	2	A36983
QY	361	SNVVTLLDDIEQWAHSE	589	2	A36983
Db	361	SNVVTLLDDIEQWAHSE	589	2	A36983

RESULT 2

JC7123

caspase-9 long chain - mouse

C/Species: Mus musculus (house mouse)

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C;Accession: JC7123
R;Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264, 550-555, 1999
A;Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9.
A;Reference number: JC7123; MUID:20001956; PMID:10529400
A;Accession: JC7123
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-454 <FUJ>
A;Cross-references: DDBJ:AB019600; NID:96440941; PID:96440942

Query Match 76.1%; Score 1658; DB 2; Length 454;
Best Local Similarity 72.5%; Pred. No. 5.1e-134;
Matches 329; Conservative 24; Mismatches 63; Indels 38; Gaps 2;

QY 1 MDEADRLRLRRCLRLVVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
DB 1 MDEADRLRLRRCLRLVVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLVT 60
QY 61 DLETRGQALPLFISCLIEDGQDMLASFLRTNRQAGL----- 98
DB 61 DLETRGQALPLFISCLIEDGQDMLASFLRTNRQAGL----- 98
QY 99 -----SKPTLENLPVLRPE-----IRKPEVLRPETPRPVDIGSGRGDVGAL 142
DB 121 AKEQVVKLPSPQAVGNLPVVLGPPELWPARKPEVLRPETPRPVDIGSGRGDVCVP 180
QY 143 ESLRGNADLAYILSMPCGCHLIINNPNFCRESGLRTRTSGNIDCEKLRFRFSSLHFWVE 202
DB 181 GKIRGNADWAYLSDPCGCHLIINNPNFCRSSGLGRTSGNIDRDKLEHFRFLRWFVE 240
QY 203 VKGDLTAKKVVALLLELARDHGDALDCCVVILSHGCOASHLQPPGAVYGTDCGCPVSVEK 262
DB 241 VKNDLTAKKVMVATLMEMAHNRHRLDCFFVVVILSHGCOASHLQPPGAVYGTDCGCVSIEK 300
QY 263 IVNIFNCTSPSLGGKPKLFFIQACGGEQKHGFEVASTSPEDSPGSNPNPDATPFQEG 322
DB 301 IVNIFNCGSPSLGGKPKLFFIQACGGEQKHGFEVACTSSQGRTLSDSEPDATPFQEG 360
QY 323 LRTPDQLDASSLTPSDIFVSYSTFPFGVSWRDPKSGSVYVETLDDIFQWHAHSEDLQS 382
DB 361 PRPLDQLDAVSSLTPSDILVSYSTFPFGVSWRDPKSGSVYIETLDGLFLQWARSDELQS 420
QY 383 LLRLVANAVSKGYTKQMPGCFNLRKKLPKTS 416
DB 421 LLRLVANAVSKGYTKQIPGCFNLRKKLPKTS 454

RESULT 3
S64710
cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster
C;Species: Crictetus griseus (Chinese hamster)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Accession: S64710; S72395
R;Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.
EMBO J. 15, 1012-1020, 1996
A;Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during
A;Reference number: S64710; MUID:9618185; PMID:8605870
A;Accession: S64710
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-277 <WAN>
A;Cross-references: EMBL:U27463
R;Wang, X.
submitted to the EMBL Data Library, May 1995
A;Reference number: S72395
A;Accession: S72395
A;Molecule type: mRNA
A;Residues: 1-79, 'A', 148-277 <WAW>
A;Cross-references: EMBL:U27463; NID:gl244443; PIDN:AA01511.1; PID:gl244444
C;Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 19.7%; Score 429; DB 2; Length 277;
Best Local Similarity 33.2%; Pred. No. 5.1e-29;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;
QY 150 DLAYILSMPCGCHLIINNPNFCRESGLRTRTSGNIDCEKLRFRFSSLHFWVEVKGLDTA 209
DB 34 DSSYKMDYPBMGVCIINNKNFHKSTGMTPRSGTDVDAAKLRFTFMNLKYEVRNKNLTLR 93
QY 210 KKMVLALLELARDHGDALDCCVVILSHGCOASHLQPPGAVYGTDCGCPVSVEKLVNIFNG 269
DB 94 EEIVELMKNASKEDHKSRSFVVCVILSHGDE-----GVIFGIDG-PIDLKLTSTYFRG 145
QY 270 TSCPSLGGKPKLFFIQACGGEQKHGFEVASTSPEDSPGSNPNPDATPFQEGRLTDPQL 329
DB 146 DRCSLIGKPKLFFIQACRGTELDGCIETDSGTEDDMT----- 183
QY 330 DATSSLTPSDIFVSYSTFPFGVSWRDPKSGSVYVETLDDIFQWHAHSEDLQSLLLRVAN 389
DB 184 --CQKIPVEADFLYASTAFGYYSWRNPKDGSFQISLCSMLKLYAHKLEFMMHILTVNR 241
QY 390 AVSVK-----GIYKMPGCFNLRKKLPF 413
DB 242 KVATEFESFLDSTFFHAKKQIPCIIVSMLTRELTF 275

RESULT 4
A55315
cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human
N;Alternate names: cysteine proteinase CPP32
C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
C;Accession: A55315; S58899; I39005
R;Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.
J. Biol. Chem. 269, 30761-30764, 1994
A;Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans
A;Reference number: A55315; MUID:95074098; PMID:7983002
A;Accession: A55315
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-277 <FER>
A;Cross-references: GB:U13737; NID:9561665; PIDN:AAA65015.1; PID:9561666
R;Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant,
Yu, V.L.; Miller, D.K.
Nature 376, 37-43, 1995
A;Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalia
A;Reference number: S58899; MUID:95319529; PMID:7596430
A;Accession: S58899
A;Molecule type: protein
A;Residues: 29-46;176-189, 'E', 191-193 <NIC>
R;Tewari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poirier
Cell 81, 801-809, 1995
A;Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease
A;Reference number: A56924; MUID:95292347; PMID:7774019
A;Accession: I39005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-189, 'E', 191-277 <RES>
A;Cross-references: EMBL:U26943; NID:9857568; PIDN:AAA74929.1; PID:9857569
C;Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 19.2%; Score 418; DB 2; Length 277;
Best Local Similarity 33.2%; Pred. No. 4.5e-28;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;
QY 150 DLAYILSMPCGCHLIINNPNFCRESGLRTRTSGNIDCEKLRFRFSSLHFWVEVKGLDTA 209
DB 34 DSSYKMDYPBMGVCIINNKNFHKSTGMTPRSGTDVDAANLRFTFMNLKYEVRNKNLTLR 93
QY 210 KKMVLALLELARDHGDALDCCVVILSHGCOASHLQPPGAVYGTDCGCPVSVEKLVNIFNG 269
DB 94 EEIVELMRDVSKEDHKSRSFVVCVLLSHGEE-----GIIFGTNG-PVDLKKITNFRG 145
QY 270 TSCPSLGGKPKLFFIQACGGEQKHGFEVASTSPEDSPGSNPNPDATPFQEGRLTDPQL 329

Db 94 BEIMELMDSVSKEDHAKRSFVCLVSHGDE-----GVIFGTNG-FVDLKKLTSEFRG 145
QY 270 TSCPSLGKPKLFIIQACGGEQKHGFEVASTSPEDSPGSPNPEDATPFQEGRLTFDQL 329
Db 146 DYCSSLTGKPKLFIIQACRGTELDGLETDSGTDEE----- 182
QY 330 DAISSLPTPSDIFVSYSTFFGFSWRDPKSGSWYVETLDDIFEQWAHSEDLSQLLRVA 389
Db 183 -ACQKIPVEADFLYATAPGYYSWRNSKDGSWFIQSLCSMLKLYAHKLEFMIHLTVNR 241
QY 390 AVSVK-----GIYKQMPGCFNFKLFF 413
Db 242 KVATEFESFLDSTFHAKKQIPCIVSMILTLYF 275

RESULT 8
A49429
interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C;Accession: A49429; T37312
R;Yuan, J.; Shaham, S.; Ledoux, S.; Ellis, H.M.; Horvitz, H.R.
Cell 75, 641-652, 1993
A;Title: The C. elegans cell death gene ced-3 encodes a protein similar to mammalian int
A;Reference number: A49429; MUID:94061982; PMID:8242740
A;Accession: A49429
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-503 <YUA>
A;Cross-references: GB:L29052; NID:G6503232; PIDN:AAA27982.2; PID:G6503233
A;Note: sequence extracted from NCBI backbone (NCBIN:139825, NCBI:P:139826)
A;Accession: T37312
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-417, 'R', 419-503 <YU2>
A;Cross-references: EMBL:L29052; PIDN:AAA27982.1
C;Genetics:
A;Gene: ced-3
A;Introns: 45/3; 94/2; 179/3; 289/3; 361/1; 403/3; 483/3

Query Match 17.8%; Score 387.5; DB 2; Length 503;
Best Local Similarity 25.0%; Pred. No. 4.1e-25;
Matches 128; Conservative 79; Mismatches 188; Indels 117; Gaps 17;
QY 1 MDEADRR-LLRRCRLRLVEELQVQLWDVLLSRLFRPHMTEDIQAGSGRRQARQLI 59
Db 1 MWRQDRRLERNIMFSSHLKVDLEILLVIAKQVLSNDGMDIN--SCGTVREKRREIV 58
QY 60 IDLETRGSOALPLFISCIETGQDMIASFLR-----TNRQAGKLS 99
Db 59 KAVQRGGVAFDAFYDALRSTGHEGLAEVLPLARSVDNSNAVEPECMPSPASHRRSRALS 118
QY 100 -----KPT-----LENLTPVVLREIRK-----PEVLRPPTP 126
Db 119 PAGYSPTRVHRDSVSSVSTSTQDIYSRARSRSRSLHSDRHNSVSPVNAFFSQP 178
QY 127 RPVDIGSGGFGDVGALES-----LRGNADLAYILSME----- 158
Db 179 SSANSSFTGCSGLGYSSSRNRSFSAKSGTQYIFHEEDMNFVDAPTISRVFDEKTYERNF 238
QY 159 --PCHCLTIINNVCRESGLRTRTGSNIDCEKLRRRFSLSLHEMVVEVKGDLTAKMWLAL 216
Db 239 SSPROMCLIIINNEHF---EQMPTTRNGTKADKNLTNLFRCMGYTVCKDNLTGRGMLTI 295
QY 217 LELAR-QDHGALDCCVVLISHGCOASHLPFGAVYTGDCPVSVEKIVNIFNGTSCPSL 275
Db 296 RDKAKHESHG--DSAILVILSHGEB-----NVIIGVDDIPISHTHEIYDILLNAANAPRL 346
QY 276 GKPKLFTIQACGGKQKHGFEVASTSPEDSPG-----SNPEPATPFQEGRLTFDQL 329
Db 347 ANKPKIVFVQACRGERRDNGFFVLDS--VDGVPAFLRGRGNDNRDGLFNFLGCVR--FQV 402

QY 330 DAI-SSLPTPSDIFVSYSTFFGFSWRDPKSGSWYVETLDDIFEQWAHSEDLSQLLRVA 388
Db 403 QQVWRKKPSQADILIIAYATTAQVSVNRNSARGSWFICAVCEVSTHAKOMDVVELLTVN 462
QY 389 NAVSV-----KGIYKQMPGCFNFKLFF 413
Db 463 KKVACGQTSQSGSNILKQWPEMTSRLKKFYF 494

RESULT 9
I67437
cysteine proteinase (EC 3.4.22.-) P32 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: I67437
R;Flaws, J.A.; Kugu, K.; Trbovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirschfield, A.N.; Tili
Endocrinology 136, 5042-5053, 1995
A;Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian ce
nuloa cells of the ovarian follicle.
A;Reference number: I53300; MUID:96042508; PMID:7588240
A;Accession: I67437
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-212 <RES>
A;Cross-references: EMBL:U34685; NID:g1004370; PIDN:AA52261.1; PID:g1004371
C;Keywords: cysteine proteinase; hydrolase

Query Match 17.6%; Score 384; DB 2; Length 212;
Best Local Similarity 33.2%; Pred. No. 2.5e-25;
Matches 79; Conservative 46; Mismatches 81; Indels 32; Gaps 3;
QY 150 DLAVLSMEPCGCHLIINNVCRESGLRTRTGSNIDCEKLRRRFSLSLHEMVVEVKGDLTA 209
Db 5 DSSYKMDYPENGLCIIINNKNFKSTGMSAENGTDVDAANLRETFMALKYEVNRKNDLTR 64
QY 210 KQVIALLELARQDHGALDCCVVLISHGCOASHLPFGAVYTGDCPVSVEKIVNIFNG 269
Db 65 BEIMELMDSVSKEDHAKRSFVCLVSHGDE-----GVIFGTNG-FVDLKKLTSEFRG 116
QY 270 TSCPSLGKPKLFIIQACGGEQKHGFEVASTSPEDSPGSPNPEDATPFQEGRLTFDQL 329
Db 117 DYCSSLTGKPKLFIIQACRGTELDGLETDSGTDEE----- 153
QY 330 DAISSLPTPSDIFVSYSTFFGFSWRDPKSGSWYVETLDDIFEQWAHSEDLSQLLRV 387
Db 154 -ACQKIPVEADFLYATAPGYYSWRNSRSGSWFIQSLCAMLKLYAHKLEFMIHLTV 210

RESULT 10
T20038
hypothetical protein C48D1.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20038
R;Burton, J.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19214
A;Accession: T20038
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-495 <WIL>
A;Cross-references: EMBL:Z81049; PIDN:CABQ2848.1; GSPDB:GN00022; CESP:C48D1.2
C;Genetics:
A;Gene: CESP:C48D1.2
A;Map position: 4
A;Introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1

Query Match 16.6%; Score 362; DB 2; Length 495;
Best Local Similarity 24.6%; Pred. No. 6.2e-23;
Matches 118; Conservative 77; Mismatches 175; Indels 110; Gaps 16;
QY 5 DRR-LLRRCRLRLVEELQVQLWDVLLSRLFRPHMTEDIQAGSGRRQARQLIIDLE 63

```
Db 4 DRSLLERNIMFSSHLKVDIEILVIAKQVLSNDGDMIN--SCGVREKRREIVKAVQ 61
QY 64 TRGSQALPLFISCLEDTGQDMLASFUR-----TNRQAGKLS----- 99
Db 62 RRGDVAFDAFYDALRSTGHEGLAEVLEPLARSVDNSNAVEFCPMSPASRRSRALSPAGY 121
QY 100 -KPT-----LENLTPVLRPEIRK-----PEVLRPETRPVVD 130
Db 122 TSSTRVHRDSVSVSFTSYQDIYSRARSRSRALHSSDRHNSPPVNAFPQSPSSAN 181
QY 131 IGSFGFGDVGALSS-----LRGNADLAYILSM-----PC 160
Db 182 SSTFGCSLGYSSRRNPSFKASGPTQYIFHEDMFVDAPTISRVDKMTYRNFSR 241
QY 161 GHCLIIINNVNFCRESGLRTRTGNIDCEKLRFRFSSLFHFMVEKGDITAKKMLALLELA 220
Db 242 GMCLIIINNEHF---EQMPTRANGTKADKDNLTNLFRCMGYTVICKDNLTGRGMLLTIRDF 298
QY 221 R-QDHGALDCCVVVILSHGCOASHLOFPFGAVYGTGDCPVSVEKIVNIFNGTSCPSLGGKP 279
Db 299 KHESHG--DSAILVILSHGEE-----NVIIIGVDDIPITSTHEIYDLLNAANAPRLANKP 349
QY 280 KLFFIQACGGEQKHGFVEASTSPEDSPG-----SNPEPDATPFOEGLRTEFDQDAI- 332
Db 350 KIVFVQACGERRDNGFPVLDS--VDGVPAFLRRGWDNRDGPLNFGVCR--PQVQVW 405
QY 333 SSLPTSDIFVSYSTPFGFVSWRDPKSGVSVETLDDIFEQWAHSEDLQSLLRVANAVS 392
Db 406 RKKPSQADILIAVATTAAQYVSWRNSARGSWFIQAVCEVFTSHAKDMVDVVELLTVKNKVA 465

RESULT 11
B54821
apoptosis regulator ICH-1, suppressive form S - human
C:Species: Homo sapiens (man)
C>Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C:Accession: B54821
R:Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
Cell 78, 739-750, 1994
A:Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulators
A:Reference number: A54821; MUID:94373811; PMID:8087842
A:Accession: B54821
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-312 <MAN>
A:Cross-references: GB:U0322
C:Keywords: alternative splicing; apoptosis
```

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Query Match 13.9%; Score 304; DB 2; Length 312;
Best Local Similarity 29.7%; Pred. No. 3.1e-18;
Matches 94; Conservative 48; Mismatches 105; Indels 70; Gaps 8;

QY 9 LRRCRLRLVEELQVLDQVLDVLLSREUFRPHMIEDIQ-RAGSGRRDQARQLIIDLETRGS 67
Db 9 LKKNRVLAKQLLSLELLEKQIITLEMBELIQAKVGSFS---QNVLLNLNLPKRGF 65
QY 68 QALPLFISCLEDTGQDMLASFRTN-----RQAGKL 98
Db 66 QAFDAFCEALRETQGHLEDMLLTTLISGLQHVLPPLSCDYDLSLPPFVCSCLYKCLR 125
QY 99 SKPTLENLT-----PVLRPEIRKPEVLRPETRPVDTGSGFGDVGALSLRGADLAY 153
Db 126 STDTHVSLNDKDGVPCLQ-----VKPCTP-----EFYQTHFQLAY 161
QY 154 ILSMPCGCHLIINNPNFCRESGLRTRTGNIDCEKLRFRFSSLFHFMVEKGDITAKKMW 213
Db 162 RLQSRPRGLAVLSNVHFTGKELBFRSGVDHSTLVTFLKLGVDVHVLCDQTAQEMQ 221
QY 214 LALLELAR--QDHGALDCCVVVILSHGCOASHLOFPFGAVYGTGDCPVSVEKIVNIFNGTSC 272
Db 222 EKLQWFAQLPAHRVTDSCIVALLSHGVE-----GAIYGVGDKLLQLQEVFQLFDNANC 274
```

```
QY 273 PSIGGPKPLFFIQACGG 289
Db 275 PSIQNKPKMFFIQACRG 291
```

RESULT 12

A46495

IL-1 beta convertase - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000

C:Accession: A46495; A47258; I48911

R:Wett, M.A.; Cerretti, D.P.; Berson, D.R.; Seavitt, J.; Gilbert, D.J.; Jenkins, N.A.; C

J. Immunol. 149, 3254-3259, 1992

A:Title: Molecular cloning of the murine IL-1 beta converting enzyme cDNA.

A:Reference number: A46495; MUID:93056487; PMID:1431103

A:Accession: A46495

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-402 <NET>

A:Cross-references: GB:I03799; NID:G198379; PIDN:AAA39306.1; PID:G198380

A:Note: sequence extracted from NCBI backbone (NCBIP:117473)

R:Molineaux, S.M.; Casano, F.J.; Rolando, A.M.; Peterson, E.P.; Limjuco, G.; Chin, J.; C

ard, A.D.; Thornberry, N.A.; Kostura, M.J., 1993

proc. Natl. Acad. Sci. U.S.A. 90, 1809-1813, 1993

A:Title: Interleukin 1 beta (IL-1 beta) processing in murine macrophages requires a stru

A:Reference number: A47258; MUID:93189587; PMID:8446594

A:Accession: A47258

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-187,189-402 <MOL>

A:Experimental source: macrophage

A:Note: sequence extracted from NCBI backbone (NCBIP:126931)

R:Casano, F.J.; Rolando, A.M.; Mudgett, J.S.; Molineaux, S.M.

Genomics 20, 474-481, 1994

A:Title: The structure and complete nucleotide sequence of the murine gene encoding inte

A:Reference number: A54264; MUID:94307735; PMID:8034321

A:Accession: I48911

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 'MAV', 7-402 <RES>

A:Cross-references: EMBL:U04269; NID:G476217; PIDN:AAA56992.1; PID:G476218

C:Genetics:

C:Introns: 6/1; 92/1; 113/1; 150/3; 208/3; 287/1; 334/1; 370/3

Query Match

Best Local Similarity 24.7%; Score 268.5; DB 2; Length 402;

Matches 110; Conservative 62; Mismatches 183; Indels 91; Gaps 16;

```
QY 7 RLRRCLRLVEELQ---VDQLMDVLLSRELFRPHMIEDIQRAGSGRRDQARQLIIDLE 63
Db 4 KILRAKQKQFINSVSGITNGLLLEKRVLNQEMDKIKLANI-TAMDKARDLCDHVS 62
QY 64 TRGSQALPLFIS---CLEDTGQDMLASF-----RTN 92
Db 63 KAGPOASQFIITYICNEDC---YLAGELOSAPSAETVATEDSKGHPSSSETKEON 119
QY 93 ROAGKLSKPTLENLTPVVRPEIRKPEVLRPETRPVDTGSGFGDVGALSLRGADLAY 152
Db 120 KEDG-----TPGLTGTCLKFCPLKAKLWKENP-----SEIYPIIMNTTRTRUA 164
QY 153 YILSMPCGCHLIINNPNFCRESGLRTRTGNIDCEKLRFRFSSLFHFMVEKGDITAKKM 212
Db 165 -----LIICNTEF---QHLSPRVGAQVDLREMKLLLEDLGYTVKVNENITALEM 210
QY 213 VLALLELAR--QDHGALDCCVVVILSHGCOASHLOFPFGAVYGTGDCPV--SVEKIVNIFNGT 270
Db 211 VKEVKEFAACPEHKTSSTFLVFMVSHGIGQEG---ICGTTYSNEVSDILKVDITFQMNTL 267
QY 271 SCPSLGGKPKLFFIQACGGEQKHGFVEASTSPEDSPGSGNPEPDATPFOEGLRT---PD 327
Db 268 KCPSLKDKPKVLIQACGEKQ--GVULLKDSVRDS-----EEDFLTDAIFE 312
QY 328 QLDAISSLPTSDIFVSYSTPFGFVSWRDPKSGVYVETLDDIFEQWAHSEDLQSLLRV 387
```


A:Molecule type: protein
A:Residues: 120-135, 'AX', 138-139, 'X', 141-142 <KRO>

C:Genetics:

A:Gene: GDB:ILLBC

A:Cross-references: GDB:132368; OMIM:147678

A:Map position: 11q23-11q23

C:Keywords: cysteine proteinase; hydrolase

```
Query Match          11.9%; Score 259; DB 2; Length 404;
Best Local Similarity 24.3%; Pred. No. 3.1e-14;
Matches 104; Conservative 62; Mismatches 176; Indels 86; Gaps 14;

QY 10 RRCLRLVELOVDLWLLSKELFRPHMIEDIORAGSGSRDQARQLIIDLETGSOA 69
   | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 10 RKLFRSMGEGINGLLDELQTRVLNKEEMKVKRE-NATVMDKTRALIDSVIPKGA 68
   | : : : | : : | : : | : : | : : | : : | : : | : : | : : |

QY 70 LPLFIS--CLED-----TCQDMLASFRLNRQAGKLSKPTLENTPVVLRPEIRKP 118
   | : : | : | : : : : : : : : : : : : : : : : : : : : : :
Db 69 CQICITYICEEDSYLAGTLGLSADQTSNYLANWQDSQGVLS-----SFPAP 114
   | : : | : | : : : : : : : : : : : : : : : : : : : : :

QY 119 EVLRPETRPVDIGSGGFDVGDALESL-----RGNADLAYILSMBPCHG-CLIIINVNFC 172
   | : : | : | : : : : : : : : : : : : : : : : : : : : :
Db 115 QAVQNPAMPETSGSGEGNVKLSLEEAQRIWKQSAEIIYPIMDKSRTRLALIIICNEEF- 173
   | : : | : | : : : : : : : : : : : : : : : : : : : : :

QY 173 RESGLRTRTGSNIDCEKLRFRFSSLFHFMVEVKGDLTAKKMWLALLELA-RQDHGALDCCV 231
   | : : | : | : : : : : : : : : : : : : : : : : : : : :
Db 174 --DSIPRTGAEVDITGMTMLLQNLGYSVDVKKNLTASDMTTELEAFARPEHKTS DSTF 231
   | : : | : | : : : : : : : : : : : : : : : : : : : : :

QY 232 VVILSHG-----COASHL-QFFGAVYGTDCFPVSVEKIVNIENGTSCTPSLGGKPKLFFIQ 285
   | : : | : | : : : : : : : : : : : : : : : : : : : : :
Db 232 LVFMSHGIREGICGKKHSEQVPDI-----LQLNAIFNMLNTKNCPSLSKDKPKVIIQ 283
   | : : | : | : : : : : : : : : : : : : : : : : : : : :

QY 286 ACGGEQKHGHFEVASTSPEDESP-----GSNPEPDATPFQEGRLTFDOLDAIS 333
   | : : | : | : : : : : : : : : : : : : : : : : : : : :
Db 284 ACRG-----DSPGVVWFKXDSVGVSGNLSLPTTEBFED-----DAIK 319
   | : : | : | : : : : : : : : : : : : : : : : : : : : :

QY 334 SLPTSDIFVSYSTPFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVANAYSV 393
   | : : | : | : : : : : : : : : : : : : : : : : : : : :
Db 320 KAHIEKDFIAFCSTFDNVSWRHPTMGSVFIGRLIEHMQEYACSCDVEIFRKVRFSFEQ 379
   | : : | : | : : : : : : : : : : : : : : : : : : : : :

QY 394 KGIYKQMP 401
   | : : | : | : : : : : : : : : : : : : : : : : : : : :
Db 380 PDGRAQMP 387
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Job time : 20 secs

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OM protein - protein search, using sw model

Run on: August 3, 2004, 08:52:15 ; Search time 41 Seconds
(without alignments)
3201.355 Million cell updates/sec

Title: US-09-961-201a-1
Perfect score: 2180
Sequence: 1 MDEADRLRLRCLRLVEEL.....YKMPGCFNLRKKLFFKTS 416

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1647	75.6	454	11	Q8C3Q9
2	1645	75.5	454	11	Q9JHK1
3	1645	75.5	454	11	Q9ROT0
4	1642	75.3	453	11	Q8C3Q0
5	1336	61.3	393	11	Q9ROS9
6	1093	50.1	383	11	Q99M88
7	1048.5	48.1	399	13	Q91B63
8	1000.5	45.9	403	13	Q90WU0
9	613	28.1	229	11	Q7TQC1
10	485	22.2	177	11	Q920G4
11	449	20.6	426	5	Q816Y2
12	443	20.3	423	13	Q91B67
13	437	20.0	313	11	Q8CHV5
14	435	20.0	316	5	Q817B0
15	424	19.4	482	11	Q9JHX4
16	421	19.3	328	5	Q81TP3

17	420	19.3	277	6	Q95ND5
18	419	19.2	277	6	Q8MJU1
19	418	19.2	280	13	Q8JGM9
20	414	19.0	452	11	O55194
21	413	18.9	280	13	Q8JG42
22	411	18.9	452	11	Q8K241
23	410	18.8	452	11	Q8C9H7
24	406	18.6	435	4	Q9BUP7
25	402.5	18.5	318	13	Q91B65
26	401	18.4	277	6	Q8MKI5
27	401	18.4	277	6	Q8MTC3
28	396	18.2	283	13	Q93417
29	393	18.0	282	13	Q98U18
30	387.5	17.8	482	13	Q90WU1
31	384	17.6	280	13	Q8JIS9
32	383.5	17.6	476	13	Q918J3
33	378.5	17.4	290	13	Q8JIS8
34	369	16.9	415	13	Q801M6
35	369	16.9	419	13	Q7ZXD2
36	362.5	16.6	303	11	O88550
37	362	16.6	182	6	O77623
38	344.5	15.8	522	4	Q8IUP5
39	333	15.3	289	5	Q86FL0
40	330.5	15.2	400	5	Q81TP2
41	330	15.1	417	5	Q9YIU6
42	326.5	15.0	304	13	Q93415
43	322	14.8	276	11	Q99M47
44	321	14.7	276	11	Q9D089
45	318	14.6	520	13	Q91B62

ALIGNMENTS

RESULT 1
Q8C3Q9 PRELIMINARY; PRT; 454 AA.
AC Q8C3Q9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 9.
GN CASP9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RC MEDLINE=22354683; PubMed=12466851;
RX The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK085095; BAC39365.1; --
DR MGD; MGI:1277950; Casp9.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016323; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASE; 1.
DR PROSITE; PS50209; CARD; 1.

DR	PROSITE; PS01122; CASPASE_CYS; 1.	
DR	PROSITE; PS01121; CASPASE_HIS; 1.	
DR	PROSITE; PS50207; CASPASE_P10; 1.	
DR	PROSITE; PS50208; CASPASE_P20; 1.	
SQ	SEQUENCE 454 AA; 49979 MW; 438A67EA6A6EE78 CRC64;	
Query Match 75.5%; Score 1647; DB 11; Length 454;		
Best Local Similarity 71.1%; Pred. No. 3.1e-139;		
Matches 325; Conservative 28; Mismatches 63; Indels 38; Gaps 2;		
QY	1 MDEADRLRRCLRLVEELQVDQLVDVLLSRELFRPHMIEDIORAGSGRRDQARQLII 60	
DB	1 MDEADRLRRCLRLVEELQVDVLLSRELFRPHMIEDIORAGSGRRDQARQLVT 60	
QY	61 DLETRGQALPLFISCLDTCQDMLASFLRTRNQAGKL----- 98	
DB	61 DLETRGQALPLFISCLDTCQDMLASFLRTRNQAGKL----- 98	
QY	99 -----SKPTLENLTPVVLRLPE-----IRKPEVLRETPTPRVDIGSGGFGDVGAL 142	
DB	121 AKQQRVVKLDPSQAVGNLTPVVLGPPELWPARLKPVEVLRETPTPRVDIGSGGHAHVCVP 180	
QY	143 ESLRGNADLAVILSMPCGCHLIINNPNFRESGLRTRTGSNIDCEKLRFRFSSLHFVME 202	
DB	181 GKIRHADMAYTLSDPCGCHLIINNPNFPCSSGLGTRTGSNLDKLEHFRWLRFVME 240	
QY	203 VKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCOASHLQFPFVGYTDCGVPVSEK 262	
DB	241 VKNDLTAKKMWLTALMEMAHRNRALDCFFVVVILSHGCOASHLQFPFVGYTDCGVSIEK 300	
QY	263 IVNIFNGTSCPSLGGKPKLFTIQACGGKQKHGFEVASTSPEDSPGSGNPEDATPTQEG 322	
DB	301 IVNIFNGSGCSLGGKPKLFTIQACGGKQKHGFEVACTSQGRTLSDSEPDVAVPTQEG 360	
QY	323 LRTEQDLDAISLTPSPDIFVSSTFPFGFVSWRDPKSGMWVETLDDIFEQWAHSEDLQS 382	
DB	361 PRPLDQLDVSSLSLTPSDILVSSTFPFGFVSWRDKKSGSWIETLDGLQEWASSEDLLQS 420	
QY	383 LLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416	
DB	421 LLLRVANAVSAKGTQKIQPGCFNLRKLPFKTS 454	
RESULT 2		
Q9JHK1	PRELIMINARY; PRT; 454 AA.	
AC	Q9JHK1	
DT	01-OCT-2000 (TrEMBLrel. 15, Created)	
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Caspase-9 (Caspase-9 long isoform).	
GN	RNCASP9.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OX	NCBT_TaxID=10116;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=SPRAGUE-DAWLEY;	
RA	Cao G., Chen D., Pei W., O'Horo C., Graham S., Simon R.P., Chen J.;	
RT	"Cloning and Characterization of Rat Caspase-9: Implication for a Role	
RT	in Neuronal Cell Death During Brain Development and Transient Cerebral	
RT	Ischemia.";	
RL	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=SPRAGUE-DAWLEY;	
RA	Itoh T., Itoh A., Pleasure D.;	
RL	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Sprague-Dawley; TISSUE=Cerebellum;	
RA	Cao G., Chen D., Graham S., Simon R.P., Chen J.;	
RT	"Cloning and Characterization of Rat Caspase-9: Implication for a Role	
RT	in Neuronal Cell Death During Brain Development and Transient Cerebral	
RT	Ischemia.";	
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.	
RN	[4]	
RP	SEQUENCE FROM N.A.	
RC	MEDLINE=21192275; PubMed=11278518;	
RA	Angelastro J.M., Moon N.Y., Liu D.X., Yang A.-S., Greene L.A.,	
RT	Frankie T.F.;	
RT	"Characterization of a Novel Caspase-9 Isoform in Rat That Inhibits	
RT	Apoptosis.";	
RL	J. Biol. Chem. 276:12190-12200 (2001).	
RN	[5]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=WKY;	
RC	MEDLINE=21552893; PubMed=11695991;	
RA	Nishiyama J., Yi X., Venkatachalam M.A., Dong Z.;	
RT	"cDNA cloning and promoter analysis of rat caspase-9.";	
RL	Biochem. J. 360:49-56 (2001).	
DR	EMBL; AF262319; AAF85658.1; -	
DR	EMBL; AF271986; AAF76217.1; -	
DR	EMBL; AF286006; AAF99705.1; -	
DR	EMBL; AF308469; AAK35159.1; -	
DR	EMBL; AY027667; AAK26235.1; -	
DR	HSP; P42574; 1PAU.	
DR	MEROPS; C14.010; -	
DR	GO; GO:0005622; C:intracellular; IEA.	
DR	GO; GO:0016329; F:apoptosis regulator activity; IEA.	
DR	GO; GO:0030693; F:caspase activity; IEA.	
DR	GO; GO:0006915; P:apoptosis; IEA.	
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.	
DR	InterPro; IPR001315; CARD.	
DR	InterPro; IPR002138; ICE_p10.	
DR	InterPro; IPR001309; ICE_p20.	
DR	InterPro; IPR002398; Peptidase_C14.	
DR	Pfam; PF00619; CARD; 1.	
DR	Pfam; PF00656; Peptidase_C14; 1.	
DR	PRINTS; PR00376; IL1BCENZYM.	
DR	SMART; SM00114; CARD; 1.	
DR	SMART; SM00115; CASc; 1.	
DR	PROSITE; PS02029; CARD; 1.	
DR	PROSITE; PS01122; CASPASE_CYS; 1.	
DR	PROSITE; PS01121; CASPASE_HIS; 1.	
DR	PROSITE; PS50207; CASPASE_P10; 1.	
DR	PROSITE; PS50208; CASPASE_P20; 1.	
SQ	SEQUENCE 454 AA; 50399 MW; 501623B29E6ED6FC CRC64;	
Query Match 75.5%; Score 1645; DB 11; Length 454;		
Best Local Similarity 71.1%; Pred. No. 4.6e-139;		
Matches 323; Conservative 32; Mismatches 61; Indels 38; Gaps 2;		
QY	1 MDEADRLRRCLRLVEELQVDQLVDVLLSRELFRPHMIEDIORAGSGRRDQARQLII 60	
DB	1 MDEADRLRRCLRLVEELQVDQLVDVLLSRELFRPHMIEDIORAGSGRRDQARQLVI 60	
QY	61 DLETRGQALPLFISCLDTCQDMLASFLRTRNQAGKL----- 98	
DB	61 DLETRGQALPLFISCLDTCQDMLASFLRTRNQAGKL----- 98	
QY	99 -----SKPTLENLTPVVLRLPE-----IRKPEVLRETPTPRVDIGSGGFGDVGAL 142	
DB	121 SKEQVVKVLDPSQALGNLTPVVLGPPELWPARLKPVEVLRETPTPRVDIGSGGHAHVCVP 180	
QY	143 ESLRGNADLAVILSMPCGCHLIINNPNFRESGLRTRTGSNIDCEKLRFRFSSLHFVME 202	
DB	181 GKIRHADMAYTLSDPCGCHLIINNPNFPCSSGLGTRTGSNLDKLEHFRWLRFVME 240	
QY	203 VKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCOASHLQFPFVGYTDCGVPVSEK 262	
DB	241 VKNDLTAKKMWLTALMEMAHRNRALDCFFVVVILSHGCOASHLQFPFVGYTDCGVSIEK 300	
QY	263 IVNIFNGTSCPSLGGKPKLFTIQACGGKQKHGFEVASTSPEDSPGSGNPEDATPTQEG 322	

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Db 301 IVNIFNGTGCPSLGGPKLFFIQACGGEQKHGFVAVFTSSQDKAFSDSEPDVAVPYQEG 360
QY 323 LRTFDQDLDAISSLPTPSDIFVSYSTFFPGFVSWRDPKSGSWYVETLDDIFFQWASEDLQS 382
Db 361 PRTLDQDLDAVSSLPTPSDILVSYSTFFPGFVSWRDPKSGSWYIETLDGVLEQWASEDLQS 420
QY 383 LLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416
Db 421 LLLRVANAVSEKGYKQIPGCFNLRKLPFKTS 454

RESULT 3
Q9ROT0
ID Q9ROT0 PRELIMINARY; PRT; 454 AA.
AC Q9ROT0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Caspase9.
GN CASP9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20001956; PubMed=10529400;
RA Fujita E., Jinbo A., Matuzaki H., Konishi H., Kikkawa U., Momoi T.;
RT "Akt phosphorylation site found in human caspase-9 is absent in mouse
caspase-9.";
RL Biochem. Biophys. Res. Commun. 264:550-555(1999).
DR EMBL; AB019600; BAA86895.1; -.
DR PIR; JC7123; JC7123.
DR HSP; P42574; 1PAU.
DR MEROPS; C14.010; -.
DR MGD; MGI:1277950; Casp9.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008915; F:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 454 AA; 50051 MW; 4614989AF923850F CRC64;

Query Match 75.5%; Score 1645; DB 11; Length 454;
Best Local Similarity 71.6%; Pred. No. 4.6e-139;
Matches 325; Conservative 28; Mismatches 63; Indels 38; Gaps 2;

QY 1 MDEARRLLRRCRLRIVEELQVDLWVLLSRELFRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEARRLLRRCRLRIVEELQVDLWVLLSRELFRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFISCLEDTGDMLASFLRTNRQAKL----- 98
Db 61 DLETRGRQALPLFISCLEDTGGTIALSLQSGRAKQDPEAVKLDHLVPLVGLPMGLT 120
QY 99 -----SKPTLENITPVVLRPE-----IRKPEVLRPTPRPVDIGSGGFDVGAL 142
Db 121 AKEQRVWKLPSQPAVGNLTPVVLGPVELWPARLKPVLRTPTPRVDIGSGGHDVCVP 180

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QY 143 ESURGNADLAIYILSMPECGHCLINNNVNFRESGLRTRTGSNIDCEKLRFRSSIHFWVE 202
Db 181 GKIRGHADMAYTLLSDPCGHLINNNVNFPCSSGLGTRTGSNLDRLKLEHFRWLRFWVE 240
QY 203 VKGDLTAKKVVALLLELARGDHALDCVWVILSHGCOASHLOFPFGAVYGTGDCPVSVEK 262
Db 241 VKNDLTAKKVVMTALMEAHENHRALDCFVVVILSHGCOASHLOFPFGAVYGTGDCSVSIEK 300
QY 263 IVNIFNGTSCPSLGGPKLFFIQACGGEQKHGFVAVFTSSQDKAFSDSEPDVAVPYQEG 322
Db 301 IVNIFNGSGCPSLGGPKLFFIQACGGEQKHGFVAVFTSSQDKAFSDSEPDVAVPYQEG 360
QY 323 LRTFDQDLDAISSLPTPSDIFVSYSTFFPGFVSWRDPKSGSWYVETLDDIFFQWASEDLQS 382
Db 361 PRTLDQDLDAVSSLPTPSDILVSYSTFFPGFVSWRDPKSGSWYIETLDGVLEQWASEDLQS 420
QY 383 LLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416
Db 421 LLLRVANAVSEKGYKQIPGCFNLRKLPFKTS 454

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RESULT 4
Q8C3Q0
ID Q8C3Q0 PRELIMINARY; PRT; 453 AA.
AC Q8C3Q0;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Caspase 9 (Fragment).
GN CASP9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/60; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK085152; BAC39378.1; -.
DR MGD; MGI:1277950; Casp9.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
FT NON TER
SQ SEQUENCE 453 AA; 49847 MW; 8F7D1C50F7ABA69F CRC64;

Query Match 75.3%; Score 1642; DB 11; Length 453;
Best Local Similarity 71.5%; Pred. No. 8.6e-139;
Matches 324; Conservative 28; Mismatches 63; Indels 38; Gaps 2;

QY 2 DEARRLLRRCRLRIVEELQVDLWVLLSRELFRPHMIEDIQAGSGSRDQARQLII 61

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Db 1 DEADQQLRRRCVRLVSELOVAELWDALLSRELFTTRDMIEDIQAGSGSRDQARQLVTD 60
QY 62 LETRGSQALPLFISCLDTSQDMLASFLRTRNQAQKL----- 98
Db 61 LETRGRQALPLFISCLDTSQGTLASLLQSGRQAQKQDPEAVKPLDHLVPVVLGPMGLTA 120
QY 99 -----SKTLENLTVPVLRPE-----IRKPEVLRPETPRPVDIGSGGFDVGALE 143
Db 121 KEORVVKLDPSPQAVGNLTVPVLPPELWPARLKPEVLRPETPRPVDIGSGGAHDVCVP 180
QY 144 SLRGNADLAYLSNPEPCGHCLINNVNFCRESGLRTRTGSNIDCEKLRFRFSSHFVVEV 203
Db 181 KIRGHADMATYLDSDPCGHCLINNVNFCPSGSLGTRTGSNLDKLEHFRWLRFVVEV 240
QY 204 KGBLTAKKMWLALLELARQDHGALDCVWVILSHGCOASHLQPPGAVYGTGDCPVSVEKI 263
Db 241 KNDLTAKKMWYALMEMAHRNRALDCFVWVILSHGCOASHLQPPGAVYGTGDCSVSIEKI 300
QY 264 VNIFNGTSCPSLGGKPKLFTQACGGEGKHGFEVASTSPDESPGNSRPRPDATPFQOGL 323
Db 301 VNIFNGSGCPSLGGKPKLFTQACGGEGKHGFEVACTSQGRITLDSDEPDVAVPYQEGP 360
QY 324 RTEQDLDAISLTPSPDIFVSYSSTFPFGVSMRDPKSGSWYVETLDDIFEQMAHSEDLQSL 383
Db 361 RPLDQLDAVSSLTPSPDILVSYSSTFPFGVSMRDKKSGSWYETLDDIGLEQWARSEDLQSL 420
QY 384 LLRVANAVSVKGIYQKMPGCFNLRKLLFFKTS 416
Db 421 LLRVANAVSAKGTYKQIPGCFNLRKLLFFKTS 453

RESULT 5
Q9ROS9
ID Q9ROS9 PRELIMINARY; PRT; 393 AA.
AC Q9ROS9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase9.
GN CASP9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20001956; PubMed=10529400;
RA Fujita E., Jinbo A., Matuzaki H., Konishi H., Kikkawa U., Momoi T.;
RT "Akt phosphorylation site found in human caspase-9 is absent in mouse
caspase-9.";
RL Biochem. Biophys. Res. Commun. 264:550-555 (1999).
DR EMBL; AB019601; BAA86896.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.010; -.
DR MGD; MGI:1277950; Casp9.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS02009; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02008; CASPASE_P20; 1.
SQ SEQUENCE 393 AA; 42975 MW; CA889475E50DD632 CRC64;
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Query Match 61.3%; Score 1336; DB 11; Length 393;
Best Local Similarity 68.8%; Pred. No. 2.2e-111;
Matches 267; Conservative 26; Mismatches 57; Indels 38; Gaps 2;

QY 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRLFRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADQLRLRCRLRLVSELQVAELMDALLSRELFTTRDMIEDIQAGSGSRDQARQLVT 60
QY 61 DLSTRSQALPLFISCLDTSQDMLASFLRTRNQAQKL----- 98
Db 61 DLSTRQALPLFISCLDTSQGTLASLLQSGRQAQKQDPEAVKPLDHLVPVVLGPMGLT 120
QY 99 -----SKTLENLTVPVLRPE-----TRKPEVLRPETPRPVDIGSGGFDVGALE 142
Db 121 AKQORVVKLEPSQAVGNLTVPVLPPELWPARLKPEVLRPETPRPVDIGSGGAHDVCVP 180
QY 143 ESLRGNADLAYIILSMPCGHCLINNVNFCRESGLRTRTGSNIDCEKLRFRFSSHFVME 202
Db 181 GKIRGHADMATYLDSDPCGHCLINNVNFCPSGSLGTRTGSNLDKLEHFRWLRFVME 240
QY 203 VKGDLTAKKMWLALLELARQDHGALDCVWVILSHGCOASHLQPPGAVYGTGDCPVSVEK 262
Db 241 VKNDLTAKKMWYALMEMAHRNRALDCFVWVILSHGCOASHLQPPGAVYGTGDCSVSIEK 300
QY 263 IVNIFNGTSCPSLGGKPKLFTQACGGEGKHGFEVASTSPDESPGNSRPRPDATPFQEG 322
Db 301 IVNIFNGSGCPSLGGKPKLFTQACGGEGKHGFEVACTSQGRITLDSDEPDVAVPYQEG 360
QY 323 LRTFDQLDAISLTPSPDIFVSYSSTFPFG 350
Db 361 PRPLDQLDAVSSLTPSPDILVSYSSTFPFG 388

RESULT 6
Q99M88
ID Q99M88 PRELIMINARY; PRT; 383 AA.
AC Q99M88;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-9 CTD isoform.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21192275; PubMed=11278518;
RA Angelastro J.M., Moon N.Y., Liu D.X., Yang A.-S., Greene L.A.,
RA Franke T.F.;
RT "Characterization of a Novel Caspase-9 Isoform in Rat That Inhibits
Apoptosis.";
RL J. Biol. Chem. 276:12190-12200 (2001).
DR EMBL; AY008275; AAG21690.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.010; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS02009; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS01122; CASPASE_HIS; 1.
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DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 383 AA; 42319 MW; 3C5D217C3100FF25 CRC64;

Query Match
Best local similarity 50.1%; Score 1093; DB 11; Length 383;
Matches 220; Conservative 22; Mismatches 47; Indels 38; Gaps 2;

QY 1 MDEADRLRLRCRLRLVEELQVDLMDVLLSRLFRPHMIEDIQRAGSGRRDQARQLII 60
Db 1 MEADRLRLRCRLRLVEELQVDLMDVLLSRLFRPHMIEDIQRAGSGRRDQARQLVI 60
QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGKL----- 98
Db 61 DLETRGQALPRFISCLDGTQDMLASFLRTNRQAGKL----- 98
QY 99 -----SKPTLENLTPVVLRLPE-----TRKPEVLRLPRLPVDIGSGFGDVGAL 142
Db 121 SKEQKVVLDPSPQALGNLTPVVLGPEELWPTLRPEVLTPETPRPVDIGSGRAHDVCTP 180
QY 143 ESLRGNADLAYILSMPCGCHLIINNVPFCRESGLTRTGSNTDCEKLRFRPSLHMVE 202
Db 181 GKIERHADWAYLTDSPCGCHLIINNVPFCPSGLSTRIGSHVDCBKLRHFCWLRFMVE 240
QY 203 VKGDLTAKKWLALALLARQDHALDCCVVVILSHGQASHLOFPQAVVGTGDCPVSVKE 262
Db 241 VKNDLTAKKWTALMEWAHRDHALDCCVVVILSHGQASHLOFPQAVVGTGDCSVSIER 300
QY 263 IVNIFNGTSCPSLGKPKLFFIIQACGG 289
Db 301 IVNIFNGTSCPSLGKPKLFFIIQACGG 327

RESULT 7
Q91B63
ID Q91B63 PRELIMINARY; PRT; 399 AA.
AC Q91B63;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Caspase-9.
GN XCASPASE-9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yaoita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase:
RT family.";
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038172; BAA94750.1; -.
DR HSP; Q15806; IQUU.
DR MEROPS; C14.010; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:001329; F:apoptosis regulator activity; IEA.
DR GO; GO:000693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR000488; Death.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILICEZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.

DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
SQ SEQUENCE 399 AA; 44772 MW; EE2A269719064F9F CRC64;

Query Match
Best local similarity 48.1%; Score 1048.5; DB 13; Length 399;
Matches 216; Conservative 67; Mismatches 113; Indels 21; Gaps 6;

QY 1 MDEADRLRLRCRLRLVEELQVDLMDVLLSRLFRPHMIEDIQRAGSGRRDQARQLII 60
Db 1 MEQELRDILRRNRRLVQLQVKELWDLVERGVFSNDMIEIQR--EGTRDQARKLLV 58
QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGKLKSKPTLENLTPVVLRLPRLPEV 120
Db 59 ELETSGQAFPLFLCLCKETAQHDLDLQSD--SGTRVLQPTPTTSP--VLKP---LPKA 113
QY 121 LRPETPRPVDIGSGFGDVGALSLRG--NADLAYILSMPCGCHLIINNVPFCRESGLR 178
Db 114 EPAEYP-----AREIRSRKGTLDKDKDYPMSDDPIGFCIIINNMFHECTGLS 161
QY 179 TGTGSNIDCEKLRRRPSLHFWVKGDLTAKKWLALALLARQDHALDCCVVVILSHG 238
Db 162 TGTGSDIDRDLKLANRMRSHFETVTKDNLTGQAMHDHLQALADQDHSQDCLLVILSHG 221
QY 239 COASHLOFPQAVVGTGDCPVSVKEIWIENGTSCPSLGKPKLFFIIQACGGKDHGFEV 298
Db 222 CETRHQFFGGVYGTGIRIPVERIVSYFNGSKPSLRKPKFIILQACGGDQKQCEV 281
QY 299 ASTSPEDSPGNNPBDATPFOGLTDFQDLDAISSLTPTSDIFVSYSFTFGFVSWRDPK 358
Db 282 TSETPLSPSTSLQSDATPVFSGEDRDEVDAVSNIPSTDILVSYSFTFGFVSWRDXH 341
QY 359 SGSWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPGCFNFKKLPFKT 415
Db 342 TGSWYVEVLDSVLAHAAADDLQSLLVWVADGVSSKGYKQIPGYFNFRLKRFYKT 398

RESULT 8
Q90WU0
ID Q90WU0 PRELIMINARY; PRT; 403 AA.
AC Q90WU0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 9 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Barton S., Bridgham J.T., Johnson A.L.;
RT "Caspase-8 and -9 expression in the hen ovary.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057940; AAL23701.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR001393; Mitoch carrier.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
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OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N;
 RA Strausberg R.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC038825; AAH38825.1; -.
 DR MGD; MGI:107739; Casp3.
 DR GO; GO:0030693; F:caspase activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; IILBCENZME.
 DR SMART; SM00115; CASc; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR Protease.
 KW NON TER
 FT NON TER
 SQ SEQUENCE 313 AA; 35174 MW; 96E98A1F04E769FC CRC64;
 Query Match 20.0%; Score 437; DB 11; Length 313;
 Best Local Similarity 31.5%; Pred. No. 9.1e-31;
 Matches 106; Conservative 52; Mismatches 123; Indels 56; Gaps 5;
 QY 87 SFLRTNRQAGKLSKPTLENLTTPVLRPEIRKPEVLRPETPRPDVIGSGFGDVGALSLR 146
 Db 21 SVLRGAWNGLRKVTENNKTSVDKSIINFEVKTHGSKSVDSGI----- 67
 QY 147 GNADLAYILSMPCGHCLINNNVFCRESGLRTRTSGNIDCEKLRFRFSSLHFVVEVKGD 206
 Db 68 -YLDSSYKMDYPENIGICIIINNNFKHSTGWSRSRGTVDAAANLRFTFMGLKYQVRNKND 126
 QY 207 LTAKKVVALLLELAROQHGALDCCVVILSHGQASHLPFGAVGTGDCGSPVSEKIVNI 266
 Db 127 LTRDILLELMDSVSKEDHKSRSFVCVILSHGDE-----GVYGTNG-FVELKLTSTF 178
 QY 267 FNGTSCPSLGGKPKLFFIQACGGEQKDHGPEVASTSPEDSPGSPNPEPDATPQEGRLTF 326
 Db 179 FRGDYCESLTGKPKLFFIQACGTGELDCGTETDSGTDEM----- 218
 QY 327 DQDLSLSTPTSDIFVSYSTFFGFSWRDPKSGSWYVETLDDIFQWHAHSEDLQSLLLR 386
 Db 219 ----ACQKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCSMLKLYAHKLEFPHILTR 274
 QY 387 VANAVSVK-----GIYKMPGCFNLRKLEF 413
 Db 275 VNRKVATEFEFSLDSTFFHAKQIPICVISMLTKEYLF 311
 RESULT 14
 Q817B0
 ID Q817B0 PRELIMINARY; PRT; 316 AA.
 AC Q817B0;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Caspase 3.
 OS Geodia cydonium (Sponge).
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
 OC Astrophorida; Geodidae; Geodia.
 OX NCBI_TaxID=6047;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wiens M., Saenger H., Kraeko A., Perovic S., Mueller W.E.G.;
 RT "Caspase-mediated apoptosis in sponges: cloning and function.";

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ417903; CAD10576.1; -.
 DR GO; GO:0030693; F:caspase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; IILBCENZME.
 DR SMART; SM00115; CASc; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR SEQUENCE 316 AA; 35319 MW; 33A46BCE6C3F9B7 CRC64;
 Query Match 20.0%; Score 435; DB 5; Length 316;
 Best Local Similarity 35.1%; Pred. No. 1.4e-30;
 Matches 113; Conservative 44; Mismatches 121; Indels 44; Gaps 9;
 QY 111 LRPEIRKPEVLRPETPRPDVIGSGFGDVGALSLRGNADLAYILSMPCGHCLINNNV 170
 Db 10 VRPLIAPTATSHPPPIPPPEEGT-----DAGRKD-----AYKMSRRPRGMALINNRN 57
 QY 171 FCRESGLRTRTSGNIDCEKLRFRFSSLHFVVEVKGDITAKKVVALLLELAROQHGALDCC 230
 Db 58 F--TCGMKERVGDGDAENLYGLFNWLGMATIRKDNLTGKATREFEDLARDHSAYDCV 115
 QY 231 VVILSHGQASHLPFGAVGTGDCGSPVSEKIVNIPTNGTSCPSLGGKPKLFFIQACGGE 290
 Db 116 VVAILTHG-----ISGRLYSTDGDLIPVEDLTKYFDGVNRPESLIGKPKVFFVQACRGG 168
 QY 291 OKDHGFEVASTSPEDSPGSPNPEPDATPQEGRLTFDQ-----LDA-----ISSLP 336
 Db 169 KFDYGVESSTDEGESVN---KETANEMME---KQFDKVVKEKALDADDETGGGYSREALP 223
 QY 337 TPSDIFVSYSTFFGFSWRDPKSGSWYVETLDDIFQWHAHSEDLQSLLLRVANAVSV--- 393
 Db 224 TEADFVLAYATVPGYYSWRNSKEYSWFIKAFVDTMRDLASKEHFMILTEVNRKVAIDFQ 283
 QY 394 -KGIIYKMPGCFNLRKLEFFK 414
 Db 284 SGRNRKQIPAPVTMLTRKLYFR 305
 RESULT 15
 Q9JHX4
 ID Q9JHX4 PRELIMINARY; PRT; 482 AA.
 AC Q9JHX4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Caspase-8.
 GN CASP8.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
 RC STRAIN=Sprague-Dawley;
 RA Itoh T., Itoh A., Pleasure D.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
 RA Cao G., Graham S.H., Chen D., Chen J.;
 RT "Molecular cloning and characterization of rat caspase-8: Its
 RT implication in delayed neuronal cell death after ischemia.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF279308; AAF87778.1; -.
 DR EMBL; AF289372; AAK83055.1; -.
 DR HSSP; Q15806; IQDU.

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DR MEROPS; C14.009; --
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILBCEZYME.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR PROSITE; PS0168; DED; 2.
SQ SEQUENCE 482 AA; 55339 MW; 82B4A29330C53264 CRC64;

Query Match      19.4%; Score 424; DB 11; Length 482;
Best Local Similarity 29.9%; Pred. No. 2.4e-29;
Matches 138; Conservative 60; Mismatches 173; Indels 90; Gaps 14;

QY 15 RLVEE--LQVDQLMDVLLSRELPRPHMEDIQRAGSGRRDQARQLIIDLETGSOALPL 72
Db 47 RLQEGMLEEDNL--SFLKELLFHSRRDLISRLVLSKSPBEMVRELQVLGKAQVAYRVM 104

QY 73 FISCLEPTGQDMLASF---LRTNRQAGKLSKPTLENLTPVLRPEIRKPEVL----- 121
Db 105 LFKLSMDMDKEDLSPKFLITIPKCKLQ---DNSLLDIFVEMEKRTILAENNLVTL 160

QY 122 -----RPETPRVDIGSGG-----FGDVGALES 145
Db 161 KSIQFRVNRSLGRIIDYERSSTERRMSTEGBELPVSVLDEVITIKQMDMWDSPGEQSE 220

QY 146 RGNADLAYILSMPEPCGHCLINNVF--CRE-----SGLRTRTGSNIDCEKLRFRFSLH 198
Db 221 SLNSDNVYQMKSPRGYCLIFNNNFSAKREDIPKLSNMEDRKGTWYDEALSKITKELH 280

QY 199 FMVEVKGLDTAKKWLALLLELARGDGHGALDCCVVWILSHGCQASHLQFGAVYGTGCPV 258
Db 281 FEIVSFSDCTASQIHEVLVSYSQSKDHGKDCFCICILSHGDK-----GIVYGTGKEA 333

QY 259 SVEKIYNIENGTSPLSGKPKLFFIQACGGEQKHGFEVASTSPEDSPGSPNPEPATP 318
Db 334 SIYELTSYFTGSKCPSLAGKPKIFFIQACQG---NNFQKAV-----PVPEDETG 378

QY 319 F-QEGLRTFDQLDAISLPTPSDIFVSYSTFPFGVSWRDPKSGSWYVETL-DDIFQWAAH 376
Db 379 LEQEHVLEEDSSSYKXVYPDEADFLGMATVKNVCVSYRDTGTGTWYIQLCSLRCRCPR 438

QY 377 SEDLQSL---LRVANAVSVKGIYKQMPGCFNLRKKLFF 413
Db 439 GEDILSILTGWYDVSNKONPRNWGMQMPIETLRKKLFF 479
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Job time : 44 secs

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OM protein - protein search, using sw model

Run on: August 3, 2004, 08:52:14 ; Search time 55 Seconds
(without alignments)
2137.087 Million cell updates/sec

Title: US-09-961-201a-1
Perfect score: 2180
Sequence: 1 MDEADRLRLRRCLRLVEEL.....YKQPGCFNLRKKLRFKTS 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2180	100.0	416	2 AAW39209	Aaw39209 Human ICE
2	2180	100.0	416	4 AAE00606	Aae00606 Human cas
3	2166	99.4	416	6 ADA10646	Ada10646 Human cas
4	2158	99.0	416	6 ADA10674	Ada10674 Human cas
5	2157	98.9	416	2 AAY21723	Aay21723 Amino aci
6	2157	98.9	416	5 ABJ01224	Abj01224 Human cas
7	2153	98.8	416	4 AAG67375	Aag67375 Amino aci
8	2153	98.8	416	4 AAU08315	Aau08315 Human asp
9	2153	98.8	416	4 AAE08938	Aae08938 Mammalian
10	2153	98.8	416	4 AAB84374	Aab84374 Amino aci
11	2153	98.8	416	6 ABB82738	Abb82738 Human cas
12	2153	98.8	416	8 ADE52020	Ade52020 Human mam
13	2150	98.6	416	6 ADA10675	Ada10675 Human cas
14	2144	98.3	416	6 ADA10676	Ada10676 Human cas
15	2069.5	94.9	401	6 ADA10677	Ada10677 Human cas
16	1288	59.1	266	4 AAE00620	Aae00620 Human cas
17	1083	43.7	203	4 AAW39208	Aaw39208 Human ICE
18	468	21.5	93	5 ABJ04760	Abj04760 Caspase-9
19	420	19.3	277	4 AAG78712	Aag78712 Pig caspa
20	418	19.2	249	3 AAB26763	Aab26763 Human cas
21	418	19.2	277	2 AAW00372	Aaw00372 Apopain C
22	418	19.2	277	2 AAW16600	Aaw16600 Apopain C
23	418	19.2	277	2 AAR95831	Aar95831 Human int
24	418	19.2	277	2 AAW00677	Aaw00677 Pro-Yana
25	418	19.2	277	2 AAW41688	Aaw41688 Amino aci

26	418	19.2	277	2 AAY21717	Aay21717 Amino aci
27	418	19.2	277	4 AAU05394	Aau05394 Human cas
28	418	19.2	277	4 AAU05395	Aau05395 Mouse cas
29	418	19.2	277	4 AAE00600	Aae00600 Human cas
30	418	19.2	277	5 ABG30904	Abg30904 Human mem
31	418	19.2	277	5 ABJ01218	Abj01218 Human cas
32	418	19.2	277	6 AAO19867	Aao19867 Bacteriop
33	418	19.2	277	7 ADD25641	Add25641 Binding d
34	418	19.2	277	7 ADE63082	Ade63082 Human Pro
35	416.5	19.1	245	4 AAB59579	Aab59579 Human cas
36	414.5	19.0	261	4 AAE00610	Aae00610 Chimeric
37	414	19.0	241	4 AAB98654	Aab98654 Caspase-3
38	414	19.0	452	7 ADB79812	Adb79812 Rat caspa
39	414	19.0	452	7 ADE63000	Ade63000 Rat Prote
40	411	18.9	452	5 ABB10110	Abb10110 Mouse cas
41	409	18.8	277	2 AAW47089	Aaw47089 Rat inter
42	409	18.8	277	7 ADE63080	Ade63080 Rat Prote
43	409	18.8	435	2 AAR66771	Aar66771 Human int
44	409	18.8	435	2 AAR98462	Aar98462 Human Ice
45	409	18.8	435	2 AAW26274	Aaw26274 Cell deat

ALIGNMENTS

RESULT 1
AAW39209
ID AAW39209 standard; peptide; 416 AA.

AC AAW39209;

XX 18-MAY-1998 (first entry)

DT Human ICE LAP-6 polypeptide.

DE ICE LAP-6; interleukin-1 beta converting enzyme apoptosis protease-6;

XX viral infection; tumour; inflammation; osteoporosis; AIDS; human;

KW Alzheimer's disease.

XX Homo sapiens.

OS EP808904-A2.

PN 26-NOV-1997.

XX 19-MAY-1997; 97EP-00303397.

PR 20-MAY-1996; 96US-0017949P.

PR 23-MAY-1996; 96US-0020344P.

XX 05-JUN-1996; 96US-0018961P.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (HUMA-) HUMAN GENOME SCI INC.

XX (UNMI) UNIV MICHIGAN.

PI Dixit VM, He W, Ruben SM, Kikly KK;

XX WPI; 1998-001790/01.

DR N-PSDB; AAW09401.

XX DNA encoding interleukin-1 beta converting enzyme apoptosis protease-6 -

PT useful to develop products to treat, e.g. viral infection, tumour,

PT Alzheimer's disease, inflammation, osteoporosis and AIDS.

XX Claim 4; Fig 1; 44pp; English.

XX This is a human interleukin-1 beta converting enzyme apoptosis protease-6

CC (ICE LAP-6) polypeptide. The ICE LAP-6 polypeptide and agonists to the

CC polypeptide can be used to induce apoptosis, e.g. as an antiviral or

CC antitumour agent, control embryonic development and tissue homeostasis

CC and the roles of such factors in dysfunction and disease. Antagonists

CC which inhibit the activity of the ICE LAP-6 polypeptide can be used to

CC treat, Alzheimer's or Parkinson's disease, rheumatoid arthritis, septic

Db 241 ASHLQPPGAVYGTGCPVSVKIVNFGTSCPSLGGKPKLFFIQAQGGKQDHGFEVAS 300
 QY 301 TSPDESPGSNPEPDATPFQGLRTFDQDLAISLPTSDIFVSYSTPPGVSWRDPKSG 360
 Db 301 TSPDESPGSNPEPDATPFQGLRTFDQDLAISLPTSDIFVSYSTPPGVSWRDPKSG 360
 QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
 Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

RESULT 3

ADA10674
 ID ADA10674 standard; protein; 416 AA.

XX AC ADA10646;

DT 06-NOV-2003 (first entry)

DE Human caspase-9 protein.

XX Human; caspase-9; anti-HIV; nootropic; neuroprotective; vasotropic;
 KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease.

XX Homo sapiens.

XX US2002160975-A1.

PN 31-OCT-2002.

XX 06-FEB-2002; 2002US-00068569.

XX 08-FEB-2001; 2001US-0267966P.

PR 24-AUG-2001; 2001US-00939293.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;

XX WPI; 2003-219992/21.

DR N-PSDB; ADA10661.

XX New nucleic acid molecules encoding a peptide or polypeptide that binds
 PT to a portion of an inhibitor of apoptosis protein, useful for inducing
 PT apoptosis and identifying inhibitors or enhancers of apoptosis for
 PT treating AIDS, or cancer.

PS Claim 36; Page 25-26; 52pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising a
 CC polynucleotide that encodes a polypeptide or peptide, or its variants
 CC that specifically binds to at least a portion of an inhibitor of
 CC apoptosis protein (IAP). Also included are a peptide or a polypeptide
 CC (comprising at least an N terminus sequence of caspase-9 N-terminal
 CC linker sequence, a first portion of a procaspase-9 that specifically
 CC binds at least a portion of an IAP and a second portion of a procaspase-9
 CC containing a mutated active site, where the peptide or polypeptide
 CC specifically binds at least a portion of an IAP and lacks cysteine
 CC protease activity, and at least a portion of caspase-3, where the peptide
 CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
 CC an IAP or an IAP Bir3 domain) or at least a portion of a mutated
 CC procaspase-9, which fails to undergo normal processing and possesses wild
 CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
 CC polynucleotide sequence that encodes the caspase-9 N-terminal linker), an
 CC expression vector comprising any of the nucleic acids, a host cell
 CC containing the expression vector, an antibody that specifically binds to
 CC the peptide or polypeptide, an antibody that specifically binds to an
 CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
 CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
 CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,

CC identifying a compound that inhibits the peptide or polypeptide
 CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
 CC a process for the manufacture of a compound for inhibiting or enhancing
 CC apoptosis in a cell. The nucleic acid molecules and peptides or
 CC polypeptides are useful for inducing apoptosis and identifying inhibitors
 CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
 CC ischaemic injury, cancer, autoimmune diseases. The present sequence
 CC represents the full length caspase-9 protein.

XX SQ Sequence 416 AA;

Query Match 99.4%; Score 2166; DB 6; Length 416;
 Best Local Similarity 99.3%; Pred. No. 3e-218;
 Matches 413; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
 Db 1 MDEADRLRLRCRLRLVEELQVQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
 QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNQAGLSKPTLENLTPVLRPEIRKPEV 120
 Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNQAGLSKPTLENLTPVLRPEIRKPEV 120
 QY 121 LRPEPRPVDIGSGGFDVGALSLRGNADLAYILSMPCGHCLIIINNVMFCRESGLRTR 180
 Db 121 LRPEPRPVDIGSGGFDVGALSLRGNADLAYILSMPCGHCLIIINNVMFCRESGLRTR 180
 QY 181 TGSNIDCEKLRERFSSILHFVVEVKGDLTAKQWVLLLELALRODHGALDCCVWILSHGCQ 240
 Db 181 TGSNIDCEKLRERFSSILHFVVEVKGDLTAKQWVLLLELALRODHGALDCCVWILSHGCQ 240
 QY 241 ASHLQPPGAVYGTGCPVSVKIVNFGTSCPSLGGKPKLFFIQAQGGKQDHGFEVAS 300
 Db 241 ASHLQPPGAVYGTGCPVSVKIVNFGTSCPSLGGKPKLFFIQAQGGKQDHGFEVAS 300
 QY 301 TSPDESPGSNPEPDATPFQGLRTFDQDLAISLPTSDIFVSYSTPPGVSWRDPKSG 360
 Db 301 TSPDESPGSNPEPDATPFQGLRTFDQDLAISLPTSDIFVSYSTPPGVSWRDPKSG 360
 QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
 Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

RESULT 4

ADA10674

ID ADA10674 standard; protein; 416 AA.

XX AC ADA10674;

XX DT 06-NOV-2003 (first entry)

XX DE Human caspase-9 protein D315A mutant.

XX Human; caspase-9; anti-HIV; nootropic; neuroprotective; vasotropic;
 KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease; mutant; mutin.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 315 /note= "Wild-type Asp substituted by Ala"

XX US2002160975-A1.

XX 31-OCT-2002.

XX 06-FEB-2002; 2002US-00068569.

PR	08-FEB-2001; 2001US-0267966P.	
PR	24-AUG-2001; 2001US-009339293.	
XX		
PA	(UYJE-) UNIV JEFFERSON THOMAS.	
XX		
PI	Alnemri ES;	
XX		
XX	WPI; 2003-219992/21.	
XX		
PT	New nucleic acid molecules encoding a peptide or polypeptide that binds	
PT	to a portion of an inhibitor of apoptosis protein, useful for inducing	
PT	apoptosis and identifying inhibitors or enhancers of apoptosis for	
PT	treating AIDS, or cancer.	
XX		
PS	Claim 36; Page; 52pp; English.	
XX		
CC	The invention relates to an isolated nucleic acid molecule comprising a	
CC	polynucleotide that encodes a polypeptide or peptide, or its variants	
CC	that specifically binds to at least a portion of an inhibitor of	
CC	apoptosis protein (IAP). Also included are a peptide or a polypeptide	
CC	(comprising at least an N terminus sequence of caspase-9 N-terminal	
CC	linker sequence, a first portion of a procaspase-9 that specifically	
CC	binds at least a portion of an IAP and a second portion of a procaspase-9	
CC	containing a mutated active site, where the peptide or polypeptide	
CC	specifically binds at least a portion of an IAP and lacks cysteine	
CC	protease activity, and at least a portion of caspase-3, where the peptide	
CC	or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by	
CC	an IAP or an IAP Bir3 domain) or at least a portion of a mutated	
CC	procaspase-9, which fails to undergo normal processing and possesses wild	
CC	type caspase-9 enzymatic activity, a nucleic acid molecule comprising a	
CC	polynucleotide sequence that encodes the caspase-9 N-terminal linker), an	
CC	expression vector comprising any of the nucleic acids, a host cell	
CC	containing the expression vector, an antibody that specifically binds to	
CC	the peptide or polypeptide, an antibody that specifically binds to an	
CC	epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis	
CC	in a cell or stimulating apoptosis in a neoplastic or tumour cell,	
CC	identifying an inhibitor or enhancer of caspase-mediated apoptosis,	
CC	identifying a compound that inhibits the peptide or polypeptide, and	
CC	producing a compound for inhibiting or enhancing apoptosis in a cell, and	
CC	a process for the manufacture of a compound for inhibiting or enhancing	
CC	apoptosis in a cell. The nucleic acid molecules and peptides or	
CC	polypeptides are useful for inducing apoptosis and identifying inhibitors	
CC	or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,	
CC	ischaemic injury, cancer, autoimmune diseases. The present sequence	
CC	represents the caspase-9 protein mutated to ablate the autocatalytic	
CC	cleavage site in the linker region. Note: the present sequence is not	
CC	shown in the specification but was created by the indexer using the	
CC	information in the claims and the wild type caspase-9 sequence.	
XX		
SQ	Sequence 416 AA;	
	Query Match 99.0%; Score 2158; DB 6; Length 416;	
	Best Local Similarity 99.0%; Pred. No. 2.1e-217;	
	Matches 412; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	
QY	1 MDEADRLRLRLRLVEELQVDLWDVLLSRLFRPHMIEDIQAGSGSRDQARQLII 60	
DB	1 MDEADRLRLRLRLVEELQVDLWDVLLSRLFRPHMIEDIQAGSGSRDQARQLII 60	
QY	61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAKLSKPTLENLTPVLRPEIRKPEV 120	
DB	61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAKLSKPTLENLTPVLRPEIRKPEV 120	
QY	121 LRPTPRPVDIGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180	
DB	121 LRPTPRPVDIGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180	
QY	181 TGSNIDCEKLRFRFSLHPWVKDGLTAKKMWLALLEARQDHGALDCCVVILSHGQQ 240	
DB	181 TGSNIDCEKLRFRFSLHPWVKDGLTAKKMWLALLEARQDHGALDCCVVILSHGQQ 240	
QY	241 ASHLOPFGAVYGTGCFVSVKEIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGEVAS 300	

Db	241 ASHLOPFGAVYGTGCFVSVKEIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGEVAS 300	
QY	301 TSPEDSPGSNPEPDATPFQEGRLRTFDQLDAISSLPDSDIFVSYSTFFGFVSWRDPKSG 360	
Db	301 TSPEDSPGSNPEPDATPFQEGRLRTFDQLDAISSLPDSDIFVSYSTFFGFVSWRDPKSG 360	
QY	361 SWYVETLDDIFEQWHAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416	
Db	361 SWYVETLDDIFEQWHAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416	
RESULT 5		
AAV21723		
ID	AAV21723 standard; protein; 416 AA.	
XX		
AC	AAV21723;	
XX		
DT	10-SEP-1999 (first entry)	
XX		
DE	Amino acid sequence of caspase-9 (ICE-LAP6).	
XX		
XX	Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;	
KW	autoimmune disease; caspase-mediated apoptosis; neurodegenerative;	
KW	tumour cell; myocardial infarction; human.	
XX		
OS	Homo sapiens.	
XX		
FN	W09935277-A2.	
XX		
PD	15-JUL-1999.	
XX		
PF	11-JAN-1999; 99WO-US000632.	
XX		
PR	09-JAN-1998; 98US-0070987P.	
XX		
PA	(UYJE-) UNIV JEFFERSON THOMAS.	
XX		
PI	Alnemri ES;	
XX		
DR	WPI; 1999-419353/35.	
XX		
DR	N-PSDB; AAX81225.	
XX		
PT	New isolated nucleic acid molecule encoding a rev-caspase - used for	
PT	screening and identifying inhibitors or enhancers for treating cancer or	
PT	autoimmune disease.	
XX		
PS	Disclosure; Fig 19A-B; 74pp; English.	
XX		
CC	The invention relates to nucleic acid molecules encoding rev-caspases.	
CC	Rev-caspases are cysteine proteases that specifically cleave proteins	
CC	after Asp residues and is expressed as a zymogen, in which the small	
CC	subunit is N-terminal to a large subunit. A gene delivery vehicle	
CC	comprising a rev-caspase coding sequence is useful for the treatment of	
CC	cancer, where the gene delivery vehicle is internalised by tumour cells.	
CC	The gene delivery vehicle can also be used to treat autoimmune diseases.	
CC	Cells transfected with a rev-caspase expressing vector can be used in	
CC	identification of inhibitors or enhancers of caspase-mediated apoptosis.	
CC	In vitro translated rev-caspase can be used to identify an inhibitor or	
CC	enhancer of caspase processing activity. Caspase inhibitors are useful	
CC	for treating neurodegenerative diseases as well as for inhibiting	
CC	apoptosis in the heart following myocardial infarction. Sequences	
CC	AAX81217 -AAX81226 represent human caspase genes encoding caspase 1-10	
CC	gene products (AAV21715-Y21724)	
XX		
SQ	Sequence 416 AA;	
	Query Match 98.9%; Score 2157; DB 2; Length 416;	
	Best Local Similarity 99.0%; Pred. No. 2.6e-217;	
	Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
QY	1 MDEADRLRLRLRLVEELQVDLWDVLLSRLFRPHMIEDIQAGSGSRDQARQLII 60	
DB	1 MDEADRLRLRLRLVEELQVDLWDVLLSRLFRPHMIEDIQAGSGSRDQARQLII 60	

CC The present sequence represents a human Mch6 polypeptide. Mch6 is a ced-3
CC homologue, and is a member of the ICE (interleukin-1-beta converting
CC enzyme) family of aspartate-specific cysteine proteases (ASCPs). The
CC specification describes a method for identifying mammalian Mch6 activity
CC modulators (inhibitors or enhancers). The compounds identified by the
CC method are useful as pharmaceuticals for treating or preventing diseases
CC characterized by increased apoptotic cell death such as Alzheimer's
CC disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis
CC pigmentosa, or cerebellar degeneration, myelodysplastic syndromes such as
CC aplastic anemia, ischemic injury including myocardial infarction, stroke
CC and reperfusion injury. The compounds are also useful for treating
CC diseases characterized by loss of apoptotic cell death such as cancers,
CC e.g. lymphomas, carcinomas and hormone dependent tumours such as breast,
CC prostate and ovarian cancer. Increased cell survival or apoptosis
CC inhibition also results in autoimmune diseases such as systemic lupus
CC erythematosus and immune-mediated glomerulonephritis as well as viral
CC infections such as herpes virus, pox virus and adenovirus and the novel
CC identified compounds are useful for treating these conditions. The Mch6
CC inhibitors are used to treat or to reduce severity of diseases
CC characterized by increased programmed cell death
XX
SQ Sequence 416 AA;

Query Match 98.8%; Score 2153; DB 4; Length 416;
Best Local Similarity 98.8%; Pred. No. 6.9e-217; Indels 0; Gaps 0;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRLFRPHMIEDIQAGSGSRDQARQLII 60
DB 1 MDEADRLRLRCRLRLVEELQVDQLMDALLSELFRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRNQAGLSKPTLENLTPVILRPEIRKPEV 120
DB 61 DLETRGSQALPLFISCLDGTQDMLASFLRNQAGLSKPTLENLTPVILRPEIRKPEV 120
QY 121 LRPETPRVDIGSGFGDVGALSLRNADLAYILSMPCGHLIINNPNFCRESGLRTR 180
DB 121 LRPETPRVDIGSGFGDVGALSLRNADLAYILSMPCGHLIINNPNFCRESGLRTR 180
QY 181 TGSNIDCEKLRFRSSPHFVEVKGDLTAKKMWLALLELAQDHGALDCCVVILSHGQQ 240
DB 181 TGSNIDCEKLRFRSSPHFVEVKGDLTAKKMWLALLELAQDHGALDCCVVILSHGQQ 240
QY 241 ASHLQFPGAVGTDCGVSVEKIVNIFNGTSCPSLGGPKLFFIOACGGEQKHGFVEAS 300
DB 241 ASHLQFPGAVGTDCGVSVEKIVNIFNGTSCPSLGGPKLFFIOACGGEQKHGFVEAS 300
QY 301 TSPDESQSNPEPDATPQEGRLTFDQDLDAISSLPTPSDIFVSYSTFFGVSWRDPKSG 360
DB 301 TSPDESQSNPEPDATPQEGRLTFDQDLDAISSLPTPSDIFVSYSTFFGVSWRDPKSG 360
QY 361 SWYVETLDDIFQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKLFKTS 416
DB 361 SWYVETLDDIFQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKLFKTS 416

RESULT 8
AAU08315
ID AAU08315 standard; protein; 416 AA.
XX
AC AAU08315;
XX
DT
XX
DE
XX
KW Human aspartate-specific cysteine protease; MCH6.
KW Human; aspartate-specific cysteine protease; MCH6; neurotropic;
KW neuroprotective; anti-Parkinsonian; anti-anemic; vasotropic; cardiant;
KW cerebroprotective; mammalian ced-3 homologue 6; gene therapy; apoptosis;
KW Alzheimer's disease; Parkinson's disease; retinitis pigmentosa;
KW cerebellar degeneration; myelodysplastic syndrome; aplastic anemia;
KW ischaemic injury; myocardial infarction; stroke; reperfusion injury;
KW amyotrophic lateral sclerosis.

XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Active-site 285..289
FT Cleavage-site 312..316
FT /label= Granzyme beta cleavage site
FT /note= "Cleavage occurs after Asp at position 315"
FT Cleavage-site 327..331
FT /label= Granzyme beta cleavage site
FT /note= "Cleavage occurs after Asp at position 330"
XX
PN US2001016345-A1.
XX
XX 23-AUG-2001.
XX 22-DEC-2000; 2000US-00746731.
XX 29-MAY-1997; 97US-00865579.
XX 25-FEB-1999; 99US-00257218.
XX
XX (ALNE/) ALNEMRI E S.
XX (FERN/) FERNANDES-ALNEMRI T.
XX (LITW/) LITWACK G.
XX
XX Alnemri ES, Fernandes-Alnemri T, Litwack G;
XX
XX WPI; 2001-535542/59.
XX N-PSDB; AAS12629.
XX
XX New Mch6 polypeptides and genes encoding the polypeptides useful for
XX diagnosing, treating or reducing the severity of cell death-mediated
XX diseases such as neurodegenerative diseases e.g. Alzheimer's disease,
XX Parkinson's disease.
XX
XX Claim 8; Fig 1; 15pp; English.
XX
XX The invention relates to an isolated gene encoding MCH6 (mammalian ced-3
XX homologue 6) an aspartate-specific cysteine protease and the MCH6
XX polypeptide. The MCH6-encoding nucleic acids and polypeptides can be used
XX to diagnose, treat (e.g. by gene therapy) or reduce the severity of cell
XX death-mediated diseases (i.e. apoptotic) such as neurodegenerative
XX diseases e.g. Alzheimer's disease, Parkinson's disease, amyotrophic
XX lateral sclerosis, retinitis pigmentosa and cerebellar degeneration, and
XX myelodysplastic syndromes, e.g. aplastic anemia, ischaemic injury,
XX myocardial infarction, stroke and reperfusion injury. The MCH6-encoding
XX nucleic acids and polypeptides can also be used to diagnose or generate
XX reagents to diagnose diseases mediated or characterised by programmed
XX cell death. A purified recombinant MCH6 protein can be used to measure
XX hydrolysis rates for various substrates such as DEVD-AMC and YVAD-AMC in
XX a continuous fluorometric assay. The present sequence represents human
XX MCH6
XX
XX Sequence 416 AA;

Query Match 98.8%; Score 2153; DB 4; Length 416;
Best Local Similarity 98.8%; Pred. No. 6.9e-217;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRLFRPHMIEDIQAGSGSRDQARQLII 60
DB 1 MDEADRLRLRCRLRLVEELQVDQLMDALLSELFRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRNQAGLSKPTLENLTPVILRPEIRKPEV 120
DB 61 DLETRGSQALPLFISCLDGTQDMLASFLRNQAGLSKPTLENLTPVILRPEIRKPEV 120
QY 121 LRPETPRVDIGSGFGDVGALSLRNADLAYILSMPCGHLIINNPNFCRESGLRTR 180
DB 121 LRPETPRVDIGSGFGDVGALSLRNADLAYILSMPCGHLIINNPNFCRESGLRTR 180
QY 181 TGSNIDCEKLRFRSSPHFVEVKGDLTAKKMWLALLELAQDHGALDCCVVILSHGQQ 240
DB 181 TGSNIDCEKLRFRSSPHFVEVKGDLTAKKMWLALLELAQDHGALDCCVVILSHGQQ 240

Db 181 TGSNIDCEKLRFRFSSPHFMVEVKGDLTAKWVLALLELAQQDHGALDCCVVVILSHGCG 240
 QY 241 ASHLQFPAGAVYGTGCPVSVKIVNIENGTSCPSLGGKPKLFFIQACGGEQKDHGFVEAS 300
 Db 241 ASHLQFPAGAVYGTGCPVSVKIVNIENGTSCPSLGGKPKLFFIQACGGEQKDHGFVEAS 300
 QY 301 TSPDESPGNSPEPDATPFQEGRLTFDQDAISSLPDPSDIFVSVSTFPFGVSWRDPKSG 360
 Db 301 TSPDESPGNSPEPDATPFQEGRLTFDQDAISSLPDPSDIFVSVSTFPFGVSWRDPKSG 360
 QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
 Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

RESULT 9

AAE08938
 ID AAE08938 standard; protein; 416 AA.

AC AAE08938;

XX 15-NOV-2001 (first entry)

DE Mammalian ced-3 homologue 6 (Mch6).

XX Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer;
 KW aspartate-specific cysteine protease; ASCP; apoptosis; therapy;
 KW autoimmune disease; cerebellar degeneration; Alzheimer's disease;
 KW cytostatic; Parkinson's disease; immunomodulator; antimicrobial;
 KW viral infection; cell death-mediated disease; neuroprotective.

XX Unidentified.

FF Key Location/Qualifiers
 FT Active-site 285..290 /note="Active site pentapeptide"
 FT Cleavage-site 315..316
 FT Cleavage-site 330..331

XX US6271361-B1.

XX 07-AUG-2001.

PF 25-FEB-1999; 99US-00257218.

XX 29-MAY-1997; 97US-00865579.

PA (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES, Fernandes-Alnemri T, Litwack G;

DR WPI; 2001-528686/58.

XX N-PSDB; AAD15656.

XX New apoptotic genes and their apoptotic protease products, useful for
 PT modulating apoptosis for the therapeutic treatment of human diseases,
 PT e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's
 PT disease.

PS Claim 2; Fig 1; 36pp; English.

XX The invention relates to an isolated gene encoding apoptotic protease,
 CC mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the aspartate-
 CC specific cysteine protease (ASCP) family. Mch6 DNA and protein sequences
 CC are useful for modulating apoptosis for the therapeutic treatment of
 CC human diseases. Mch6 sequences are useful for upregulating apoptosis
 CC (e.g. for treating cancers, autoimmune disease or viral infections) or
 CC downregulating apoptosis (e.g. for treating Alzheimer's disease,
 CC Parkinson's disease or cerebellar degeneration). The Mch6 sequence is
 CC useful for diagnosing, treating or reducing the severity of cell death-
 CC mediated diseases, as well as other diseases mediated by either increased
 CC or decreased programmed cell death. The present amino acid sequence is
 CC Mch6

XX SQ

Sequence 416 AA;

Query Match

Best Local Similarity 98.8%; Score 2153; DB 4; Length 416;

Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRRCLRLVEELQVDQDLWDVLLSRLFRPHMIEDIORAGSGSRDQARQLII 60

Db 1 MDEADRLRLRRCLRLVEELQVDQDLWDVLLSRLFRPHMIEDIORAGSGSRDQARQLII 60

QY 61 DLETGSGQALPLFTISCLDGTQDMLASFLRTRNQAQKLSKPTLENLTPVWLRPEIRKPEV 120

Db 61 DLETGSGQALPLFTISCLDGTQDMLASFLRTRNQAQKLSKPTLENLTPVWLRPEIRKPEV 120

QY 121 LRPEPRPVDIGSGGFGDVGALSLRGNADLAYILSMPECHGLIINNVPFCRESGLRTR 180

Db 121 LRPEPRPVDIGSGGFGDVGALSLRGNADLAYILSMPECHGLIINNVPFCRESGLRTR 180

QY 181 TGSNIDCEKLRFRFSSPHFMVEVKGDLTAKWVLALLELAQQDHGALDCCVVVILSHGCG 240

Db 181 TGSNIDCEKLRFRFSSPHFMVEVKGDLTAKWVLALLELAQQDHGALDCCVVVILSHGCG 240

QY 241 ASHLQFPAGAVYGTGCPVSVKIVNIENGTSCPSLGGKPKLFFIQACGGEQKDHGFVEAS 300

Db 241 ASHLQFPAGAVYGTGCPVSVKIVNIENGTSCPSLGGKPKLFFIQACGGEQKDHGFVEAS 300

QY 301 TSPDESPGNSPEPDATPFQEGRLTFDQDAISSLPDPSDIFVSVSTFPFGVSWRDPKSG 360

Db 301 TSPDESPGNSPEPDATPFQEGRLTFDQDAISSLPDPSDIFVSVSTFPFGVSWRDPKSG 360

QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

RESULT 10

AAE84374

ID AAE84374 standard; protein; 416 AA.

AC AAE84374;

DT 22-AUG-2001 (first entry)

DE Amino acid sequence of aspartate-specific cysteine protease Mch6.

XX Human; apoptotic protease; Mch6; aspartate-specific cysteine protease;
 KW cell death; cancer; autoimmune disease; systemic lupus erythematosus;
 KW viral infection; degenerative disorder; Alzheimer's disease;
 KW Parkinson's disease; myelodysplastic syndrome; myocardial infarction;
 KW stroke.

XX Homo sapiens.

XX US2001006779-Al.

XX 05-JUL-2001.

PF 29-MAY-1997; 97US-00865579.

XX 29-MAY-1997; 97US-00865579.

XX (ALNE/) ALNEMRI E S.

PA (FERN/) FERNANDES-ALNEMRI T.

XX (LITW/) LITWACK G.

PI Alnemri ES, Fernandes-Alnemri T, Litwack G;

XX WPI; 2001-389294/41.

XX N-PSDB; AAE25191.

XX Isolated gene encoding a human apoptotic protease known as Mch6, useful
 PT in the diagnosis or treatment of cell death-mediated conditions, e.g.

PT cancers and autoimmune diseases such as systemic lupus erythematosus.

XX Claim 8; Fig 1A-C; 15pp; English.

XX The present sequence represents a human apoptotic protease, designated
XX Mch6. Mch6 is an aspartate-specific cysteine protease. Mch6 polypeptides
XX and polynucleotides can be used to diagnose, treat or reduce the severity
XX of cell death-mediated conditions, e.g. cancers, autoimmune diseases such
XX as systemic lupus erythematosus, viral infections such as herpesvirus,
XX degenerative disorders such as Alzheimer's disease and Parkinson's
XX disease, myelodysplastic syndromes such as myocardial infarction and
XX stroke. They can also be used to screen for compounds that inhibit or
XX promote Mch6 mediated apoptosis

XX SQ Sequence 416 AA;

Query Match 98.8%; Score 2153; DB 4; Length 416;
Best Local Similarity 98.8%; Pred. No. 6.9e-217;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLRLVEELQVDQMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Qy 61 DLETRGSAQLPLFISCLDGTQDMLASFLRNQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSAQLPLFISCLDGTQDMLASFLRNQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Qy 121 LRPTPRPVDIGSGFGDVGALSLRGNADLAYILSMPCGCHLIINNVPFCRESGLRTR 180
Db 121 LRPTPRPVDIGSGFGDVGALSLRGNADLAYILSMPCGCHLIINNVPFCRESGLRTR 180
Qy 181 TGSNIDCEKLRRLRRSSSHFVVEKGLTAKKMWLALLELAQDHDGALDCCVWVILSHGCG 240
Db 181 TGSNIDCEKLRRLRRSSSHFVVEKGLTAKKMWLALLELAQDHDGALDCCVWVILSHGCG 240
Qy 241 ASHLQFPGAVYGTDCGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQCAGGEQKHGFEVAS 300
Db 241 ASHLQFPGAVYGTDCGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQCAGGEQKHGFEVAS 300
Qy 301 TSPDESFGSNPEPDATPFQGLRFTDQDLSLPTSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQGLRFTDQDLSLPTSDIFVSYSTPFGFVSWRDPKSG 360
Qy 361 SWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 11
ABB82738 standard; protein; 416 AA.

XX ABB82738;
XX AC ABB82738;
XX 07-MAR-2003 (first entry)
XX Human caspase-9 polypeptide.
XX Caspase-9; TUCAN; cancer; biomarker; cIAP2; Apaf1; Bcl-2; Smac; human.
XX Homo sapiens.
XX OS
XX PN WO200290931-A2.
XX PD 14-NOV-2002.
XX PF 07-MAY-2002; 2002WO-US014487.
XX XX
XX 07-MAY-2001; 2001US-0289223P.
XX PR 12-FEB-2002; 2002US-0356934P.
XX XX
XX (BURN-) BURNHAM INST.

XX Reed JC;

XX WPI; 2003-111999/10.

XX Determining a prognosis for survival for a cancer patient, useful for
XX determining if the patient is at risk for relapse, comprises measuring a
XX level of TUCAN in a sample from the patient, and comparing it to a
XX reference level.

XX Example; Page 125-126; 153pp; English.

XX The invention relates to determining a prognosis for survival for a
XX cancer patient. The method involves (a) measuring a level of a tumour up-
XX regulated CARD-containing antagonist of caspase-9 (TUCAN) in a neoplastic
XX cell-containing sample from the cancer patient; and (b) comparing the
XX level of TUCAN in the sample to a reference level of TUCAN, where a low
XX level of TUCAN in the sample correlates with increased survival of the
XX patient. Alternatively, the method involves measuring levels of TUCAN and
XX one or more biomarkers selected from the group of cIAP2, Apaf1, Bcl-2, or
XX Smac in a neoplastic cell-containing sample from the cancer patient. The
XX method is useful for determining if the patient is at risk for relapse,
XX or for determining a proper course of treatment for a patient with
XX cancer. The method is also useful for monitoring the effectiveness of a
XX course of treatment for a patient with cancer, e.g. colon cancer,
XX gastrointestinal cancer, breast cancer, ovarian cancer, lung cancer,
XX leukemia, CNS cancer, melanoma, prostate cancer, or renal cancer. The
XX present sequence represents a human caspase-9 polypeptide

XX SQ Sequence 416 AA;

Query Match 98.8%; Score 2153; DB 6; Length 416;
Best Local Similarity 98.8%; Pred. No. 6.9e-217;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLRLVEELQVDQMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Qy 61 DLETRGSAQLPLFISCLDGTQDMLASFLRNQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSAQLPLFISCLDGTQDMLASFLRNQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Qy 121 LRPTPRPVDIGSGFGDVGALSLRGNADLAYILSMPCGCHLIINNVPFCRESGLRTR 180
Db 121 LRPTPRPVDIGSGFGDVGALSLRGNADLAYILSMPCGCHLIINNVPFCRESGLRTR 180
Qy 181 TGSNIDCEKLRRLRRSSSHFVVEKGLTAKKMWLALLELAQDHDGALDCCVWVILSHGCG 240
Db 181 TGSNIDCEKLRRLRRSSSHFVVEKGLTAKKMWLALLELAQDHDGALDCCVWVILSHGCG 240
Qy 241 ASHLQFPGAVYGTDCGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQCAGGEQKHGFEVAS 300
Db 241 ASHLQFPGAVYGTDCGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQCAGGEQKHGFEVAS 300
Qy 301 TSPDESFGSNPEPDATPFQGLRFTDQDLSLPTSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQGLRFTDQDLSLPTSDIFVSYSTPFGFVSWRDPKSG 360
Qy 361 SWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 12
ADE52020 standard; protein; 416 AA.

XX ADE52020;
XX AC ADE52020;
XX 29-JAN-2004 (first entry)
XX Human mammalian ced-3 homologue 6 (Mch6).

cytostatic; virucide; nootropic; neuroprotective; antiparkinsonian; cardiant; apoptosis modulator; aspartate-specific cysteine protease; gene therapy; aspartate-specific cysteine protease agonist; aspartate-specific cysteine protease antagonist; Mch6; mammalian ced-3 homologue 6; apoptosis; cancer; viral infection; degenerative disorder; Alzheimers disease; Parkinsons disease; myocardial infarction; human; mammalian ced-3 homologue 6; Mch6.

OS Homo sapiens.

XX US2002183504-A1.

XX 05-DEC-2002.

XX 29-JAN-2002; 2002US-00059749.

XX 29-MAY-1997; 97US-00865579.

XX 25-FEB-1999; 99US-00257218.

XX 22-DEC-2000; 2000US-00746731.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES, Fernandes-Alnemri T, Litwack G; WPI; 2004-040943/04.

XX New isolated gene encoding a mammalian ced-3 homologue 6, for modulating apoptosis for the therapeutic treatment of human diseases, such as cancers and degenerative disorders.

XX Claim 8; SEQ ID NO 2; 15pp; English.

XX The invention describes an isolated gene (I) encoding Mch6 (mammalian ced-3 homologue 6), or a functional fragment of it. (I) And the polypeptide encoded by (I) is used to modulate apoptosis for the therapeutic treatment of human diseases. (I) Is used to prepared a recombinant aspartate-specific cysteine protease, that it encodes. The recombinant protease can be used to screen for Mch6 inhibitors. Disorders involving apoptosis that can be diagnosed or treated by (I) or the polypeptide it encodes, including cancers, viral infections, degenerative disorders, such as Alzheimers and Parkinsons disease, and myocardial infarction. This is the amino acid sequence of human mammalian ced-3 homologue 6 (Mch6), a member of the aspartate-specific cysteine protease (ASCP) family of proteases.

XX Sequence 416 AA;

Query Match
Best Local Similarity 98.8%; Score 2153; DB 8; Length 416;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEQLVDQLMDVLLSRELFRPHMEDIQAGSGSRDQARQLII 60

DB 1 MDEADRLRLRCRLRLVEQLVDQLMDVLLSRELFRPHMEDIQAGSGSRDQARQLII 60

QY 61 DLETRGSQALPLFISCLETTGDMLASFLTRNRQAKLSKPTLENLTPVLRPEIRKPKV 120

DB 61 DLETRGSQALPLFISCLETTGDMLASFLTRNRQAKLSKPTLENLTPVLRPEIRKPKV 120

QY 121 LRPETPRVDIGSGFGDVGALSLRGNADLAVILSMPECGHCLINNVNFCRESGLRTR 180

DB 121 LRPETPRVDIGSGFGDVGALSLRGNADLAVILSMPECGHCLINNVNFCRESGLRTR 180

QY 181 TGSNIDCEKLRFRSSLHFMVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGQQ 240

DB 181 TGSNIDCEKLRFRSSLHFMVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGQQ 240

QY 241 ASHLOFPGAVGTDCGQSVSEKIVNIFNGTSCPSLGGKPKLFFIQACGEQKDHGFVAS 300

DB 241 ASHLOFPGAVGTDCGQSVSEKIVNIFNGTSCPSLGGKPKLFFIQACGEQKDHGFVAS 300

QY 301 TSPDESFGSNPEPDATPFQGLRFTDQLDAISSLPTSDIFVSVSTPFGVSWEDPKSG 360

DB 301 TSPDESFGSNPEPDATPFQGLRFTDQLDAISSLPTSDIFVSVSTPFGVSWEDPKSG 360

QY 361 SWYVETLDDIFEWAHSEDLQSLLLRVANAVSVKGIYKQMGCFNFKLFFKTS 416

DB 361 SWYVETLDDIFEWAHSEDLQSLLLRVANAVSVKGIYKQMGCFNFKLFFKTS 416

RESULT 13

ADA10675

ID ADA10675 standard; protein; 416 AA.

XX ADA10675;

XX 06-NOV-2003 (first entry)

XX Human caspase-9 protein D315A/D330A mutant.

XX Human; caspase-9; anti-HIV; nootropic; neuroprotective; vasotropic; cytostatic; immunosuppressive; inhibitor of apoptosis protein; IAP; caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3; Bir3 domain; apoptosis; AIDS; neurodegenerative disease; ischaemic injury; cancer; autoimmune disease; mutant; muten.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 315 /note= "Wild-type Asp substituted by Ala"

XX Misc-difference 330 /note= "Wild-type Asp substituted by Ala"

XX US2002160975-A1.

XX 31-OCT-2002.

XX 06-FEB-2002; 2002US-00068569.

XX 08-FEB-2001; 2001US-0267966P.

XX 24-AUG-2001; 2001US-00939293.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;

XX WPI; 2003-219992/21.

XX New nucleic acid molecules encoding a peptide or polypeptide that binds to a portion of an inhibitor of apoptosis protein, useful for inducing apoptosis and identifying inhibitors or enhancers of apoptosis for treating AIDS, or cancer.

XX Claim 37; Page; 52pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising a polynucleotide that encodes a polypeptide or peptide, or its variants that specifically binds to at least a portion of an inhibitor of apoptosis protein (IAP). Also included are a peptide or a polypeptide (comprising at least an N terminus sequence of caspase-9 N-terminal linker sequence, a first portion of an IAP and a second portion of a procaspase-9 containing a mutated active site, where the peptide or polypeptide specifically binds at least a portion of an IAP and lacks cysteine protease activity, and at least a portion of caspase-3, where the peptide or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by an IAP or an IAP Bir3 domain) or at least a portion of a mutated procaspase-9, which fails to undergo normal processing and possesses wild type caspase-9 enzymatic activity, a nucleic acid molecule comprising a polynucleotide sequence that encodes the caspase-9 N-terminal linker, an expression vector comprising any of the nucleic acids, a host cell containing the expression vector, an antibody that specifically binds to the peptide or polypeptide, an antibody that specifically binds to an

CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
CC identifying a compound that inhibits the peptide or polypeptide,
CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
CC a process for the manufacture of a compound for inhibiting or enhancing
CC apoptosis in a cell. The nucleic acid molecules and peptides or
CC polypeptides are useful for inducing apoptosis and identifying inhibitors
CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
CC ischaemic injury, cancer, autoimmune diseases. The present sequence
CC represents the caspase-9 protein mutated to ablate the autocatalytic
CC cleavage site in the linker region. Note: the present sequence is not
CC shown in the specification but was created by the indexer using the
CC information in the claims and the wild type caspase-9 sequence.
XX
XX
SQ Sequence 416 AA;

Query Match 98.6%; Score 2150; DB 6; Length 416;
Best Local Similarity 98.8%; Pred. No. 1.4e-216;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGLSKPTLENLTPVLRPEIRKPEV 60
DB 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGLSKPTLENLTPVLRPEIRKPEV 60
QY 61 DLETRGSQALPLFISCLDTPGDMLASFLRTNRQAGLSKPTLENLTPVLRPEIRKPEV 120
DB 61 DLETRGSQALPLFISCLDTPGDMLASFLRTNRQAGLSKPTLENLTPVLRPEIRKPEV 120
QY 121 LRPTPRVDITGSGFGDVGALSLRGADLAYILSMFPCGHLIINNVCRESGLR 180
DB 121 LRPTPRVDITGSGFGDVGALSLRGADLAYILSMFPCGHLIINNVCRESGLR 180
QY 181 TGSNIDCEKLRRLRRSFLHFMVEVKGDLTAKXWVLLALLEARQDHGALDCCVVLISHGQC 240
DB 181 TGSNIDCEKLRRLRRSFLHFMVEVKGDLTAKXWVLLALLEARQDHGALDCCVVLISHGQC 240
QY 241 ASHLQFPAGVGTDCPVSVEKIVNIENGTSFSGKPKLFFIOACGGEQKHGHFEVAS 300
DB 241 ASHLQFPAGVGTDCPVSVEKIVNIENGTSFSGKPKLFFIOACGGEQKHGHFEVAS 300
QY 301 TSPDESFGSNPEPATPFQGLRTFDQDLAISSLTPTSDIFVSYSTPFGFVSWDRPKSG 360
DB 301 TSPDESFGSNPEPATPFQGLRTFDQDLAISSLTPTSDIFVSYSTPFGFVSWDRPKSG 360
QY 361 SWYVETLDDIFQWAHSEDLQSLLRVANAVSVKGIYQMPGCFNLRKLPFKTS 416
DB 361 SWYVETLDDIFQWAHSEDLQSLLRVANAVSVKGIYQMPGCFNLRKLPFKTS 416

RESULT 14
ADA10676
ID ADA10676 standard; protein; 416 AA.

XX AC ADA10676;

XX DT 06-NOV-2003 (first entry)

XX DE Human caspase-9 protein E306A/D315A/D330A mutant.

XX KW Human; caspase-9; anti-HIV; neurotropic; neuroprotective; vasotropic;
XX KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
XX KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
XX KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
XX KW ischaemic injury; cancer; autoimmune disease; mutant; mutein.

XX OS Synthetic.
XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT FT Misc-difference 306

FT FT /note= "Wild-type Glu substituted by Ala"

FT FT Misc-difference 315

FT FT /note= "Wild-type Asp substituted by Ala"
FT FT Misc-difference 330
XX XX /note= "Wild-type Asp substituted by Ala"
PN PN US2002160975-A1.
XX XX 31-OCT-2002.
XX XX 06-FEB-2002; 2002US-00068569.
XX XX 08-FEB-2001; 2001US-0267966P.
XX XX 24-AUG-2001; 2001US-00939293.
XX XX (UJVE-) UNIV JEFFERSON THOMAS.
XX XX Alnemri ES;
XX XX WPI; 2003-219992/21.
XX XX
PT PT New nucleic acid molecules encoding a peptide or polypeptide that binds
PT PT to a portion of an inhibitor of apoptosis protein, useful for inducing
PT PT apoptosis and identifying inhibitors or enhancers of apoptosis for
PT PT treating AIDS, or cancer.
XX XX
PS Claim 38; Page; 52pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising a
CC polynucleotide that encodes a polypeptide or peptide, or its variants
CC that specifically binds to at least a portion of an inhibitor of
CC apoptosis protein (IAP). Also included are a peptide or a polypeptide
CC (comprising at least an N terminus sequence of caspase-9 N-terminal
CC linker sequence, a first portion of a procaspase-9 that specifically
CC binds at least a portion of an IAP and a second portion of a procaspase-9
CC containing a mutated active site, where the peptide or polypeptide
CC specifically binds at least a portion of an IAP and lacks cysteine
CC protease activity, and at least a portion of caspase-3, where the peptide
CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
CC an IAP or an IAP Bir3 domain) or at least a portion of a mutated
CC procaspase-9, which fails to undergo normal processing and possesses wild
CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
CC polynucleotide sequence that encodes the caspase-9 N-terminal linker, an
CC expression vector comprising any of the nucleic acids, a host cell
CC containing the expression vector, an antibody that specifically binds to an
CC the peptide or polypeptide, an antibody that specifically binds to an
CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
CC producing a compound that inhibits the peptide or polypeptide,
CC a process for the manufacture of a compound for inhibiting or enhancing
CC apoptosis in a cell. The nucleic acid molecules and peptides or
CC polypeptides are useful for inducing apoptosis and identifying inhibitors
CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
CC ischaemic injury, cancer, autoimmune diseases. The present sequence
CC represents the caspase-9 protein mutated to ablate the autocatalytic
CC cleavage site in the linker region. Note: the present sequence is not
CC shown in the specification but was created by the indexer using the
CC information in the claims and the wild type caspase-9 sequence.

XX SQ Sequence 416 AA;

Query Match 98.3%; Score 2144; DB 6; Length 416;
Best Local Similarity 98.6%; Pred. No. 6.1e-216;
Matches 410; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGLSKPTLENLTPVLRPEIRKPEV 60
DB 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGLSKPTLENLTPVLRPEIRKPEV 60
QY 61 DLETRGSQALPLFISCLDTPGDMLASFLRTNRQAGLSKPTLENLTPVLRPEIRKPEV 120
DB 61 DLETRGSQALPLFISCLDTPGDMLASFLRTNRQAGLSKPTLENLTPVLRPEIRKPEV 120

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QY 121 LRPEPRVDIGSGGFDVGALSLRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180
Db |||
QY 121 LRPEPRVDIGSGGFDVGALSLRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180
Db |||
QY 181 TGSNIDCEKLRRLRFSLSHFVVEKGDLTAKKMWLALLELARQDHGALDCCVVILSHGCO 240
Db |||
QY 181 TGSNIDCEKLRRLRFSLSHFVVEKGDLTAKKMWLALLELARQDHGALDCCVVILSHGCO 240
Db |||
QY 241 ASHLQFPGAVYGTDCGCPVSVEKIVNIENGTSCLPSLGGKPKLFFITQACGGQKHGFVEAS 300
Db |||
QY 241 ASHLQFPGAVYGTDCGCPVSVEKIVNIENGTSCLPSLGGKPKLFFITQACGGQKHGFVEAS 300
Db |||
QY 301 TSPEDSPGNSNPEPATPFQEGRLTFDQLDAISLPTSPDIFVSYSTFFGVSWRDPKSG 360
Db |||
QY 301 TSPEDSPGNSNPEPATPFQEGRLTFDQLDAISLPTSPDIFVSYSTFFGVSWRDPKSG 360
Db |||
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
Db |||
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
Db |||
```

RESULT 15

ADAL0677
ID ADAL0677 standard; protein; 401 AA.

XX AC ADAL0677;

XX DT 06-NOV-2003 (first entry)

XX DE Human caspase-9 protein del316-330 mutant.

XX KW Human; caspase-9; anti-HIV; nootropic; neuroprotective; vasotropic;
KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
KW ischaemic injury; cancer; autoimmune disease; mutant; muten.

XX OS Synthetic.
XX SS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 315..316
XX FT /note= "Residues 316-330 of the wild-type protein have
XX been deleted"

XX EN US2002160975-A1.

XX PD 31-OCT-2002.

XX PF 06-FEB-2002; 2002US-00068569.

XX PR 08-FEB-2001; 2001US-0267966P.

XX PR 24-AUG-2001; 2001US-00939293.

XX PA (UYJE-) UNIV JEFFERSON THOMAS.

XX PI Alnewri ES;

XX DR WPI; 2003-219992/21.

XX FT New nucleic acid molecules encoding a peptide or polypeptide that binds
XX to a portion of an inhibitor of apoptosis protein, useful for inducing
XX apoptosis and identifying inhibitors or enhancers of apoptosis for
XX treating AIDS, or cancer.

XX PS Claim 39; Page: 52pp; English.

XX CC The invention relates to an isolated nucleic acid molecule comprising a
XX polynucleotide that encodes a polypeptide or peptide, or its variants
XX that specifically binds to at least a portion of an inhibitor of
XX apoptosis protein (IAP). Also included are a peptide or a polypeptide
XX (comprising at least an N terminus sequence of caspase-9 N-terminal
XX linker sequence, a first portion of a procaspase-9 that specifically

CC binds at least a portion of an IAP and a second portion of a procaspase-9
CC containing a mutated active site, where the peptide or polypeptide
CC specifically binds at least a portion of an IAP and lacks cysteine
CC protease activity, and at least a portion of caspase-3, where the peptide
CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
CC an IAP or an IAP Bir3 domain) or at least a portion of a mutated
CC procaspase-9, which fails to undergo normal processing and possesses wild
CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
CC polynucleotide sequence that encodes the caspase-9 N-terminal linker, an
CC expression vector comprising any of the nucleic acids, a host cell
CC containing the expression vector, an antibody that specifically binds to
CC the peptide or polypeptide, an antibody that specifically binds to an
CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
CC in a cell or stimulating apoptosis in a neoplastic or tumor cell,
CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
CC identifying a compound that inhibits the peptide or polypeptide,
CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
CC a process for the manufacture of a compound for inhibiting or enhancing
CC apoptosis in a cell. The nucleic acid molecules and peptides or
CC polypeptides are useful for inducing apoptosis and identifying inhibitors
CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
CC ischaemic injury, cancer, autoimmune diseases. The present sequence
CC represents the caspase-9 protein mutated to ablate the autocatalytic
CC cleavage site in the linker region. Note: the present sequence is not
CC shown in the specification but was created by the indexer using the
CC information in the claims and the wild type caspase-9 sequence.

XX
SQ Sequence 401 AA;

Query Match 94.9%; Score 2069.5; DB 6; Length 401;
Best Local Similarity 95.7%; Pred. No. 3.9e-208;
Matches 398; Conservative 1; Mismatches 2; Indels 15; Gaps 1;

QY 1 MDEADRLRRCLRLVEELQVDQDWLLSLRLEPHEMIEDIQRAGSSRRDQARQLII 60
Db |||

QY 1 MDEADRLRRCLRLVEELQVDQDWLLSLRLEPHEMIEDIQRAGSSRRDQARQLII 60
Db |||

QY 61 DLETRGSQALPLFISCLDTGQDMLASFLRTNRQAGLSKPTLENTLPVLRPEIRKPEV 120
Db |||

QY 61 DLETRGSQALPLFISCLDTGQDMLASFLRTNRQAGLSKPTLENTLPVLRPEIRKPEV 120
Db |||

QY 121 LRPEPRVDIGSGGFDVGALSLRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180
Db |||

QY 121 LRPEPRVDIGSGGFDVGALSLRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180
Db |||

QY 181 TGSNIDCEKLRRLRFSLSHFVVEKGDLTAKKMWLALLELARQDHGALDCCVVILSHGCO 240
Db |||

QY 181 TGSNIDCEKLRRLRFSLSHFVVEKGDLTAKKMWLALLELARQDHGALDCCVVILSHGCO 240
Db |||

QY 241 ASHLQFPGAVYGTDCGCPVSVEKIVNIENGTSCLPSLGGKPKLFFIACGGEQKHGFVEAS 300
Db |||

QY 241 ASHLQFPGAVYGTDCGCPVSVEKIVNIENGTSCLPSLGGKPKLFFIACGGEQKHGFVEAS 300
Db |||

QY 301 TSPEDSPGNSNPEPATPFQEGRLTFDQLDAISLPTSPDIFVSYSTFFGVSWRDPKSG 360
Db |||

QY 301 TSPEDSPGNSNPEPATPFQEGRLTFDQLDAISLPTSPDIFVSYSTFFGVSWRDPKSG 360
Db |||

QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
Db |||

QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 401
Db |||

Search completed: August 3, 2004, 08:53:23
Job time : 57 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 08:54:46 ; Search time 45 Seconds
(without alignments)
2899.824 Million cell updates/sec

Title: US-09-961-201a-1

Perfect score: 2180

Sequence: 1 MDEADRLRLRCRLRLVEEL.....YKMPGCFNLRKLFKTS 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pap.*
- 2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pap.*
- 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pap.*
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- 10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pap.*
- 11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pap.*
- 12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pap.*
- 13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pap.*
- 14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pap.*
- 15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pap.*
- 16: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pap.*
- 17: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pap.*
- 18: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2166	99.4	416	13	US-10-068-569-1	Sequence 1, Appli
2	2157	98.9	416	9	US-09-954-697-30	Sequence 30, Appl
3	2153	98.8	416	10	US-09-851-873-102	Sequence 102, App
4	2153	98.8	416	12	US-09-746-731-2	Sequence 2, Appli
5	2153	98.8	416	13	US-10-059-743-2	Sequence 4, Appli
6	2153	98.8	416	14	US-10-141-618-4	Sequence 4, Appli
7	1282	58.8	266	15	US-10-116-275-172	Sequence 172, App
8	773	35.5	159	12	US-10-424-599-174531	Sequence 174531,
9	468	21.5	93	13	US-10-014-269-27	Sequence 27, Appl
10	468	21.5	93	13	US-10-002-974-27	Sequence 27, Appl
11	468	21.5	93	14	US-10-314-506-27	Sequence 27, Appl
12	419	19.2	277	15	US-10-155-567-4	Sequence 4, Appli
13	418	19.2	264	13	US-10-103-448-3	Sequence 3, Appli
14	418	19.2	264	13	US-10-108-929-3	Sequence 3, Appli
15	418	19.2	277	9	US-09-895-263-4	Sequence 4, Appli

16	418	19.2	277	9	US-09-954-697-12	Sequence 12, Appl
17	418	19.2	277	10	US-09-851-873-98	Sequence 98, Appl
18	418	19.2	277	12	US-10-232-884-4	Sequence 4, Appli
19	418	19.2	277	14	US-10-214-932-108	Sequence 108, App
20	418	19.2	277	14	US-10-207-655-202	Sequence 202, App
21	418	19.2	277	14	US-10-280-670-5	Sequence 5, Appli
22	418	19.2	277	15	US-10-368-438-30	Sequence 30, Appl
23	418	19.2	277	16	US-10-408-765A-172	Sequence 172, App
24	418	19.2	277	16	US-10-701-490-11	Sequence 11, Appl
25	414	19.0	452	14	US-10-205-219-52	Sequence 52, Appl
26	409.5	18.8	284	12	US-10-232-884-5	Sequence 5, Appli
27	409.5	18.8	451	9	US-09-888-243-28	Sequence 28, Appl
28	409	18.8	421	15	US-10-368-438-10	Sequence 10, Appl
29	409	18.8	435	8	US-08-459-455-51	Sequence 51, Appl
30	409	18.8	435	9	US-09-954-697-9	Sequence 9, Appli
31	409	18.8	435	10	US-09-851-873-97	Sequence 97, Appl
32	409	18.8	435	14	US-10-280-670-9	Sequence 9, Appli
33	409	18.8	441	8	US-08-459-455-43	Sequence 43, Appl
34	401.5	18.4	505	9	US-09-888-243-5	Sequence 5, Appli
35	395.5	18.1	503	8	US-08-459-455-36	Sequence 36, Appl
36	395.5	18.1	503	14	US-10-123-529-8	Sequence 8, Appli
37	390.5	17.9	464	15	US-10-368-438-18	Sequence 18, Appl
38	385.5	17.7	503	8	US-08-459-455-2	Sequence 2, Appli
39	385.5	17.7	503	9	US-09-888-243-29	Sequence 29, Appl
40	385.5	17.7	503	14	US-10-280-670-10	Sequence 10, Appl
41	385	17.7	457	12	US-10-296-115-1281	Sequence 1281, Ap
42	383	17.6	479	9	US-09-410-194-20	Sequence 20, Appl
43	383	17.6	479	10	US-09-851-873-101	Sequence 101, App
44	383	17.6	479	15	US-10-368-438-7	Sequence 7, Appli
45	383	17.6	496	12	US-10-232-884-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-10-068-569-1
; Sequence 1, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-1

Query Match	99.4%;	Score 2166;	DB 13;	Length 416;
Best Local Similarity	99.3%;	Pred. No. 1.2e-206;		
Matches 413;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	MDEADRLRLRCRLRLVEELQVQMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII	60	
Db	1	MDEADRLRLRCRLRLVEELQVQMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII	60	
QY	61	DLETRGSQALPLFTSCLEDTGQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV	120	
Db	61	DLETRGSQALPLFTSCLEDTGQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV	120	
QY	121	LRPETPRVDIGSGFGDVGALSLRGNADLAYILSMPCGCHLIINNVCRESGLTR	180	
Db	121	LRPETPRVDIGSGFGDVGALSLRGNADLAYILSMPCGCHLIINNVCRESGLTR	180	
QY	181	TGSNIDCEKLRRRFSSLFHVMVEKGLDTAKQWVLLALLELARQDRGALDCCVVVILSHGCQ	240	


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; FILING DATE: 22-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-746-731-2

Query Match          98.8%; Score 2153; DB 12; Length 416;
Best Local Similarity 98.8%; Pred. No. 2.3e-205;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRVEELQVDLWDVLLSRFLFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCRLRVEELQVDLWDVLLSRFLFRPHMIEDIQAGSGRRDQARQLII 60
QY 61 DLETGSQLPLFISCLEDTGQDMLASFRTNRQAGKLSKPTLENLTPVVLREIRKPEV 120
Db 61 DLETGSQLPLFISCLEDTGQDMLASFRTNRQAGKLSKPTLENLTPVVLREIRKPEV 120
QY 121 LRPETPRPVDIGSGGFDVGALESFRTNRQAGKLSKPTLENLTPVVLREIRKPEV 180
Db 121 LRPETPRPVDIGSGGFDVGALESFRTNRQAGKLSKPTLENLTPVVLREIRKPEV 180
QY 181 TGSNDICEKLRRFSSHPFVVEKGLTAKKMWLALLELARQDHGALDCCVVILSHGCQ 240
Db 181 TGSNDICEKLRRFSSHPFVVEKGLTAKKMWLALLELARQDHGALDCCVVILSHGCQ 240
QY 241 ASHLQFPGAVYGTGDCPVSVKEIVNIFNGTSCPSLGKPKLFIQACGGEQKDHGFVAS 300
Db 241 ASHLQFPGAVYGTGDCPVSVKEIVNIFNGTSCPSLGKPKLFIQACGGEQKDHGFVAS 300
QY 301 TSPEDESPGSNPEPDATPFQEGRLTFDQLDAISSLTPSDIFVSYSTFFPGFVSWRDPKSG 360
Db 301 TSPEDESPGSNPEPDATPFQEGRLTFDQLDAISSLTPSDIFVSYSTFFPGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLILRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLQSLILRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 5
US-10-059-749-2
; Sequence 2, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emdad S.
; Fernandes-Alnemri, Teresa
; Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-059-749-2

Query Match          98.8%; Score 2153; DB 13; Length 416;
Best Local Similarity 98.8%; Pred. No. 2.3e-205;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRVEELQVDLWDVLLSRFLFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCRLRVEELQVDLWDVLLSRFLFRPHMIEDIQAGSGRRDQARQLII 60
QY 61 DLETGSQLPLFISCLEDTGQDMLASFRTNRQAGKLSKPTLENLTPVVLREIRKPEV 120
Db 61 DLETGSQLPLFISCLEDTGQDMLASFRTNRQAGKLSKPTLENLTPVVLREIRKPEV 120
QY 121 LRPETPRPVDIGSGGFDVGALESFRTNRQAGKLSKPTLENLTPVVLREIRKPEV 180
Db 121 LRPETPRPVDIGSGGFDVGALESFRTNRQAGKLSKPTLENLTPVVLREIRKPEV 180
QY 181 TGSNDICEKLRRFSSHPFVVEKGLTAKKMWLALLELARQDHGALDCCVVILSHGCQ 240
Db 181 TGSNDICEKLRRFSSHPFVVEKGLTAKKMWLALLELARQDHGALDCCVVILSHGCQ 240
QY 241 ASHLQFPGAVYGTGDCPVSVKEIVNIFNGTSCPSLGKPKLFIQACGGEQKDHGFVAS 300
Db 241 ASHLQFPGAVYGTGDCPVSVKEIVNIFNGTSCPSLGKPKLFIQACGGEQKDHGFVAS 300
QY 301 TSPEDESPGSNPEPDATPFQEGRLTFDQLDAISSLTPSDIFVSYSTFFPGFVSWRDPKSG 360
Db 301 TSPEDESPGSNPEPDATPFQEGRLTFDQLDAISSLTPSDIFVSYSTFFPGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLILRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLQSLILRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 6
US-10-141-618-4
; Sequence 4, Application US/10141618
; Publication No. US20030165887A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods For Determining the Prognosis
; TITLE OF INVENTION: For Cancer Patients Using Tucan
; FILE REFERENCE: P-LJ 5254
; CURRENT APPLICATION NUMBER: US/10/141,618
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,233
; PRIOR FILING DATE: 2001-05-07
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; PRIOR APPLICATION NUMBER: US 60/356,934
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US 09/389,221
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-141-618-4

Query Match          98.8%; Score 2153; DB 14; Length 416;
Best Local Similarity 98.8%; Pred. No. 2.3e-205;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRRCLRLVEELQVDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 1 MDEADRLRRCLRLVEELQVDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 60

QY 61 DLETRGSQALPLFTSCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSQALPLFTSCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120

QY 121 LRPTPRPVDIGSGGFGDVGALSLRGADLAYILSMPEPCGHCLIIINNVPFCRESGLRTR 180
Db 121 LRPTPRPVDIGSGGFGDVGALSLRGADLAYILSMPEPCGHCLIIINNVPFCRESGLRTR 180

QY 181 TGSNIDCEKLRRRFPSSLFHFVVEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCQ 240
Db 181 TGSNIDCEKLRRRFPSSLFHFVVEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCQ 240

QY 241 ASHLQFPQAVYGTGCPVSEKIVINFGTSCPSLGGKPKLFFTOACGGEOKDHGFVEAS 300
Db 241 ASHLQFPQAVYGTGCPVSEKIVINFGTSCPSLGGKPKLFFTOACGGEOKDHGFVEAS 300

QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLSLPTPSDIFVSYSTFPFGFVSRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLSLPTPSDIFVSYSTFPFGFVSRDPKSG 360

QY 361 SWYVETLDDIPEQWAHSEDLSQLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
Db 361 SWYVETLDDIPEQWAHSEDLSQLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416

RESULT 7
US-10-116-275-172
; Sequence 172, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20067
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-172

Query Match          59.8%; Score 1282; DB 15; Length 266;
Best Local Similarity 63.2%; Pred. No. 7.1e-119;
Matches 263; Conservative 0; Mismatches 3; Indels 150; Gaps 1;
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QY 1 MDEADRLRRCLRLVEELQVDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 180
Db 1 MDEADRLRRCLRLVEELQVDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 60

QY 61 DLETRGSQALPLFTSCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSQALPLFTSCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120

QY 121 LRPTPRPVDIGSGGFGDVGALSLRGADLAYILSMPEPCGHCLIIINNVPFCRESGLRTR 180
Db 121 LRPTPRPVDIGSGGFGDV----- 139

QY 181 TGSNIDCEKLRRRFPSSLFHFVVEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCQ 240
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QY 241 ASHLQFPQAVYGTGCPVSEKIVINFGTSCPSLGGKPKLFFTOACGGEOKDHGFVEAS 300
Db 140 -----EOKDHGFVEAS 150

QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLSLPTPSDIFVSYSTFPFGFVSRDPKSG 360
Db 151 TSPDESFGSNPEPDATPFQEGRLTFDQDLSLPTPSDIFVSYSTFPFGFVSRDPKSG 210

QY 361 SWYVETLDDIPEQWAHSEDLSQLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 416
Db 211 SWYVETLDDIPEQWAHSEDLSQLLLRVANAVSVKGIYKQMPGCFNFKLFFKTS 266

RESULT 8
US-10-424-599-174531
; Sequence 174531, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 174531
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_12861C.1.pep
US-10-424-599-174531

Query Match          35.5%; Score 773; DB 12; Length 159;
Best Local Similarity 96.9%; Pred. No. 1.7e-68;
Matches 154; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY 1 MDEADRLRRCLRLVEELQVDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 180
Db 1 MDEADRLRRCLRLVEELQVDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 60

QY 61 DLETRGSQALPLFTSCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSQALPLFTSCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120

QY 121 LRPTPRPVDIGSGGFGDVGALSLRGADLAYILSMPE 159
Db 121 LRPTPRPVDIGSGGFGDVGASESLRGADLAYILSMPE 159

RESULT 9
US-10-014-269-27
; Sequence 27, Application US/10014269
; Publication No. US20020127673A1
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; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogur, Yasunori
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06645
; CURRENT APPLICATION NUMBER: US/10/014,269
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-269-27

Query Match 21.5%; Score 468; DB 13; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.9e-38;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNR 93
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNR 93

RESULT 10
US-10-002-974-27
; Sequence 27, Application US/10002974
; Publication No. US20020197616A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogur, Yasunori
; APPLICANT: Cho, Judy
; APPLICANT: Nicolae, Dan I.
; APPLICANT: Bonen, Denise
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06646
; CURRENT APPLICATION NUMBER: US/10/002,974
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-974-27

Query Match 21.5%; Score 468; DB 13; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.9e-38;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNR 93
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNR 93

RESULT 11
US-10-314-506-27
; Sequence 27, Application US/10314506
; Publication No. US20030175762A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogura, Yasunori

; TITLE OF INVENTION: Modulators of NOD2 Signaling
; FILE REFERENCE: UM-06984
; CURRENT APPLICATION NUMBER: US/10/314,506
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 10,014,269
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/244,289
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-314-506-27

Query Match 21.5%; Score 468; DB 14; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.9e-38;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNR 93
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNR 93

RESULT 12
US-10-155-567-4
; Sequence 4, Application US/10155567
; Publication No. US20030219421A1
; GENERAL INFORMATION:
; APPLICANT: CHRISTAKOS, Sylvia
; TITLE OF INVENTION: CALBINDIN-D 28K PROTECTION AGAINST GLUCOCORTICOID INDUCED CELL DEATH
; FILE REFERENCE: 267/266
; CURRENT APPLICATION NUMBER: US/10/155,567
; CURRENT FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 277
; TYPE: PRT
; ORGANISM: homosapiens
US-10-155-567-4

Query Match 19.2%; Score 419; DB 15; Length 277;
Best Local Similarity 33.2%; Pred. No. 7.4e-33;
Matches 91; Conservative 50; Mismatches 91; Indels 42; Gaps 4;

QY 150 DLAYILSMPEPCGHCLIIINNVCRESGLTRTGSNIDCEKLRFRSSLIHFVVEVKGDLTA 209
Db 34 DTGYKMDYEMGLCLIIINNKNFKSTGMTSGTSDVDAANLRETFRNLKYEVNRKNDLTR 93

QY 210 KKMVLALLELARQDHGALDCCVVVILSHGCOASHLQFPGAVYGTGCPVSVKIVNIENG 269
Db 94 EEIIVLMRDVSKEDSKRSSFFCVLLSHGEE-----GIIFGTNG-PVDLKKITNFFRG 145

QY 270 TSCPSLGGKPKLFFFTQACGGEQKDGHGFVASTSPDESPSGNPEPDATPFQGLRTFDQL 329
Db 146 DRCRSLTGKPKLFIQACRGTELDGCIETDSGVDDM----- 182

QY 330 DAISLPLTPSDIFVSYSTFGFVSWRDPKSGSWYVETLLDIFEQWHAHSDLOSLLLRVAN 389
Db 183 -ACHKIPVDADFLYAYSTAPGYISWNSKSGSWFTQSLCAMLKQYADKLEFMHILTRVNR 241

QY 390 AVSVK-----GIYKQMPGCENFLRKILFF 413
Db 242 KVATEFESFSPDATPHAKKQIPCIVSMILTKELYF 275

RESULT 13

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US-10-103-448-3
; Sequence 3, Application US/10103448
; Publication No. US20020155579A1
; GENERAL INFORMATION:
; APPLICANT: Krebs, Joseph F.
; APPLICANT: Srinivasan, Anu
; APPLICANT: Fritz, Lawrence C.
; APPLICANT: Wu, Joseph C.
; TITLE OF INVENTION: MEMBRANE DERIVED CASPASE-3, COMPOSITIONS
; TITLE OF INVENTION: COMPRISING THE SAME AND METHODS OF USE THEREFOR
; FILE REFERENCE: 480140.468D1
; CURRENT APPLICATION NUMBER: US/10/103,448
; CURRENT FILING DATE: 2002-03-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-103-448-3

Query Match      19.2%; Score 418; DB 13; Length 264;
Best Local Similarity 33.2%; Pred. No. 8.6e-33;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAYILSMPCGCHLIINNPNFCRESGLRTRTGSNIDCEKLRFRFSSLHFVMEVKGDLTA 209
Db 21 DNSYKMDYPENGLCIIINNKNFKSTGTSRSGTVDVDAANLRETFRNKLYEVRNKNDLTR 80

QY 210 KKMVLALLELARODHGALDCVWVILSHGCOASHLQFPFGAVYGTGDCPVSVEKIVNIFNG 269
Db 81 EEIVELMRDVSKEHSHKRSFVCLVSHGEE-----GIIFGTNG-FVDLKKITNFRPG 132

QY 270 TSCPSLGKPKLFFIQACGGQKHGFEVASTSPEDSPGNSNPEPDATPFQEGRLTFDQL 329
Db 133 DRCRSLTGKPKLFFIQACRGTELDGCIETDSGVDDM----- 169

QY 330 DAISLPTPSDIFVSYSTFGFVSWRDPKSGSWVETLDDIFEQWASEDLQSLLLRVAN 389
Db 170 -ACHKIPVDADFLYAYSTAGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFPHILTRVNR 228

QY 390 AVSVK-----GIYKMPGCGFNFLRKKLFF 413
Db 229 KVATEFESFSDATFHAKKQIPCIVSMLTKEYLF 262

RESULT 15
US-09-895-263-4
; Sequence 4, Application US/09895263
; Patent No. US20020076793A1
; GENERAL INFORMATION:
; APPLICANT: He, Wei-Wu et al.
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
; TITLE OF INVENTION: Like Apoptosis Protease 3 and 4
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/895,263
; FILING DATE: 02-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jonathan L. Klein
; REGISTRATION NUMBER: 41,119
; REFERENCE/DOCKET NUMBER: PF140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-251-6015
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-895-263-4

Query Match      19.2%; Score 418; DB 9; Length 277;
Best Local Similarity 33.2%; Pred. No. 9.3e-33;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAYILSMPCGCHLIINNPNFCRESGLRTRTGSNIDCEKLRFRFSSLHFVMEVKGDLTA 209
Db 34 DNSYKMDYPENGLCIIINNKNFKSTGTSRSGTVDVDAANLRETFRNKLYEVRNKNDLTR 93
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 08:52:20 ; Search time 19 Seconds
(without alignments)
1130.337 Million cell updates/sec

Title: US-09-961-201A-1
Perfect score: 2180
Sequence: 1 MDEADRLRLRLVEEL.....YKQMPGCCFNLRKKLFFKTS 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

.listing first 45 summaries

Database :

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2180	100.0	416	3	US-08-852-936C-1
2	2180	100.0	416	3	US-09-300-328-1
3	2180	100.0	416	4	US-09-069-023-23
4	2157	98.9	416	4	US-09-561-756-30
5	2157	98.9	416	4	US-09-227-721-30
6	2157	98.9	416	4	US-09-354-697-30
7	2153	98.8	416	3	US-09-257-218-2
8	2153	98.8	416	3	US-09-311-760-2
9	2153	98.8	416	4	US-08-865-579-2
10	2153	98.8	416	4	US-10-059-749-2
11	1083	49.7	203	3	US-08-852-936C-4
12	1083	49.7	203	3	US-09-300-328-4
13	418	19.2	277	3	US-08-591-605-2
14	418	19.2	277	3	US-08-964-308-6
15	418	19.2	277	3	US-08-462-969B-4
16	418	19.2	277	3	US-08-964-313-6
17	418	19.2	277	4	US-09-069-138-6
18	418	19.2	277	4	US-09-561-756-12
19	418	19.2	277	4	US-09-227-721-12
20	418	19.2	277	4	US-08-383-503-30
21	418	19.2	277	4	US-09-124-934A-4
22	418	19.2	277	4	US-08-724-378D-5
23	418	19.2	277	4	US-08-334-251D-4
24	418	19.2	277	4	US-09-516-747-30
25	418	19.2	277	4	US-09-954-697-12
26	418	19.2	277	5	PCT-US96-10521-30
27	417	19.1	277	4	US-09-291-289-11

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Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 51, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 2, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 44, Appl
Sequence 43, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 4, Appli
Sequence 5, Appli

28 409 18.8 277 2 US-08-890-542A-2
29 409 18.8 421 4 US-08-983-502-10
30 409 18.8 421 4 US-09-516-747-10
31 409 18.8 421 5 PCT-US96-10521-10
32 409 18.8 435 3 US-08-258-287B-53
33 409 18.8 435 3 US-08-368-704C-51
34 409 18.8 435 4 US-09-561-756-9
35 409 18.8 435 4 US-09-227-721-9
36 409 18.8 435 4 US-08-816-075-2
37 409 18.8 435 4 US-08-724-378D-9
38 409 18.8 435 4 US-09-954-697-9
39 409 18.8 441 3 US-08-258-287B-44
40 409 18.8 441 3 US-08-368-704C-43
41 408 18.7 277 3 US-08-964-308-10
42 408 18.7 277 3 US-08-964-313-10
43 408 18.7 277 4 US-09-069-138-10
44 405 18.6 435 5 PCT-US94-07127A-4
45 401.5 18.4 505 2 US-08-394-189B-5

ALIGNMENTS

RESULT 1
US-08-852-936C-1
; Sequence 1, Application US/08852936C
; Patent No. 6010878
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.
; APPLICANT: RUBEN, STEVEN M.
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
; TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
; NUMBER OF INVENTIONS: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,936C
; FILING DATE: 08-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/018,961
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: 60/020,344
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: 60/017,949
; FILING DATE: 20-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: p50483-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-852-936C-1
Query Match      100.0%; Score 2180; DB 3; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.3e-230;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 60
DB 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 60
QY 61 DLETRGSOALPLFISCLDTQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
DB 61 DLETRGSOALPLFISCLDTQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
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DB 121 LRPTPRPVDITGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNPNFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRSSSLHFMVVEKGLTAKKMWLALLLELARDQDHGALDCCVVVILSHGCQ 240
DB 181 TGSNIDCEKLRRLRRSSSLHFMVVEKGLTAKKMWLALLLELARDQDHGALDCCVVVILSHGCQ 240
QY 241 ASHLQFPGAVGTGDCPVSVKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
DB 241 ASHLQFPGAVGTGDCPVSVKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQGLRTFDQDAISSLPTSDIFVSVSTFPFGVSWRDPKSG 360
DB 301 TSPDESFGSNPEPDATPFQGLRTFDQDAISSLPTSDIFVSVSTFPFGVSWRDPKSG 360
QY 361 SWIVETLDDIPEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
DB 361 SWIVETLDDIPEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 2
US-09-300-328-1
; Sequence 1, Application US/09300328
; Patent No. 6294169
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.
; APPLICANT: RUBEN, STEVEN M.
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
; TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/300,328
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,936
; FILING DATE: 08-MAY-1997
; APPLICATION NUMBER: 60/018,961
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: 60/020,344
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: 60/017,949
; FILING DATE: 20-MAY-1996
; ATTORNEY/AGENT INFORMATION:

NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: P50483-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-300-328-1
Query Match      100.0%; Score 2180; DB 3; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.3e-230;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 60
DB 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 60
QY 61 DLETRGSOALPLFISCLDTQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
DB 61 DLETRGSOALPLFISCLDTQDMLASFLRTNRQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 121 LRPTPRPVDITGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNPNFCRESGLRTR 180
DB 121 LRPTPRPVDITGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNPNFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRSSSLHFMVVEKGLTAKKMWLALLLELARDQDHGALDCCVVVILSHGCQ 240
DB 181 TGSNIDCEKLRRLRRSSSLHFMVVEKGLTAKKMWLALLLELARDQDHGALDCCVVVILSHGCQ 240
QY 241 ASHLQFPGAVGTGDCPVSVKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
DB 241 ASHLQFPGAVGTGDCPVSVKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQGLRTFDQDAISSLPTSDIFVSVSTFPFGVSWRDPKSG 360
DB 301 TSPDESFGSNPEPDATPFQGLRTFDQDAISSLPTSDIFVSVSTFPFGVSWRDPKSG 360
QY 361 SWIVETLDDIPEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
DB 361 SWIVETLDDIPEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 3
US-09-069-023-23
; Sequence 23, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-069-023-23
Query Match      100.0%; Score 2180; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.3e-230;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVLRPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVLRPEIRKPEV 120
QY 121 LRPEPRPVDIGSGGFDVGALESLRGNADLAYILSMPECGHCLIIINNVMFCRESGLRTR 180
Db 121 LRPEPRPVDIGSGGFDVGALESLRGNADLAYILSMPECGHCLIIINNVMFCRESGLRTR 180
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Db 181 TGSNIDCEKLRRLRRFSSLHFMVEVKDGLTAKKMWLALLELARQDHGALDCCVWVILSHGCQ 240
QY 241 ASHLQFPGAVYGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300
Db 241 ASHLQFPGAVYGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300
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Db 301 TSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLSQLLLRVANAVSVKGIYKQMPGCNFFLRKKLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLSQLLLRVANAVSVKGIYKQMPGCNFFLRKKLFFKTS 416

RESULT 4

US-09-561-756-30
; Sequence 30, Application US/09561756
; Patent No. 6376226
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/561.756
; PRIOR FILING DATE: 2000-04-26
; PRIOR FILING DATE: 09/227,721
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-561-756-30

Query Match 98.9%; Score 2157; DB 4; Length 416;
Best Local Similarity 99.0%; Pred. No. 1.7e-227;
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFPRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVLRPEIRKPEV 120
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QY 181 TGSNIDCEKLRRLRRFSSLHFMVEVKDGLTAKKMWLALLELARQDHGALDCCVWVILSHGCQ 240
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QY 241 ASHLQFPGAVYGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300

Db 241 ASHLQFPGAVYGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLSQLLLRVANAVSVKGIYKQMPGCNFFLRKKLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLSQLLLRVANAVSVKGIYKQMPGCNFFLRKKLFFKTS 416

RESULT 5

US-09-227-721-30
; Sequence 30, Application US/09227721
; Patent No. 6379950
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/227,721
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-227-721-30

Query Match 99.9%; Score 2157; DB 4; Length 416;
Best Local Similarity 99.0%; Pred. No. 1.7e-227;
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFPRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFPRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVLRPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVLRPEIRKPEV 120
QY 121 LRPEPRPVDIGSGGFDVGALESLRGNADLAYILSMPECGHCLIIINNVMFCRESGLRTR 180
Db 121 LRPEPRPVDIGSGGFDVGALESLRGNADLAYILSMPECGHCLIIINNVMFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRFSSLHFMVEVKDGLTAKKMWLALLELARQDHGALDCCVWVILSHGCQ 240
Db 181 TGSNIDCEKLRRLRRFSSLHFMVEVKDGLTAKKMWLALLELARQDHGALDCCVWVILSHGCQ 240
QY 241 ASHLQFPGAVYGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300
Db 241 ASHLQFPGAVYGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLSQLLLRVANAVSVKGIYKQMPGCNFFLRKKLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLSQLLLRVANAVSVKGIYKQMPGCNFFLRKKLFFKTS 416

RESULT 6

US-09-954-697-30
; Sequence 30, Application US/09954697
; Patent No. 6610541
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697

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; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-30

Query Match      98.9%; Score 2157; DB 4; Length 416;
Best Local Similarity 99.0%; Pred. No. 1.7e-227;
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGSRDQARQLII 60
DB 1 MDEADRLRLRCRLRLVEELQVDQLMDALLSELFRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGKLSKPTLENLTPVWLRLPEIRKPEV 120
DB 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGKLSKPTLENLTPVWLRLPEIRKPEV 120
QY 121 LRPETPRPVDIGSGFGDVGALSLRGNADLAYILSMPCGCHLIINNPNFCRESGLRTR 180
DB 121 LRPETPRPVDIGSGFGDVGALSLRGNADLAYILSMPCGCHLIINNPNFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRSSPHFVEVKGDLTAKXWVLLALLEARQDHGALDCCVVVILSHGQ 240
DB 181 TGSNIDCEKLRRLRRSSPHFVEVKGDLTAKXWVLLALLEARQDHGALDCCVVVILSHGQ 240
QY 241 ASHLQFPGAVGTDCPVSVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
DB 241 ASHLQFPGAVGTDCPVSVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
QY 301 TSPEDSPGNSPEPDATPFQGLRTFDQLDAISSLPTSPDIFVSYSTPFGFVSWDRPKSG 360
DB 301 TSPEDSPGNSPEPDATPFQGLRTFDQLDAISSLPTSPDIFVSYSTPFGFVSWDRPKSG 360
QY 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLFKTS 416
DB 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLFKTS 416

RESULT 7
US-09-257-218-2
; Sequence 2, Application US/09257218
; Patent No. 6271361
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,218
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-257-218-2

Query Match      98.8%; Score 2153; DB 3; Length 416;
Best Local Similarity 98.8%; Pred. No. 4.8e-227;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGSRDQARQLII 60
DB 1 MDEADRLRLRCRLRLVEELQVDQLMDALLSELFRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGKLSKPTLENLTPVWLRLPEIRKPEV 120
DB 61 DLETRGSQALPLFISCLDGTQDMLASFLRTNRQAGKLSKPTLENLTPVWLRLPEIRKPEV 120
QY 121 LRPETPRPVDIGSGFGDVGALSLRGNADLAYILSMPCGCHLIINNPNFCRESGLRTR 180
DB 121 LRPETPRPVDIGSGFGDVGALSLRGNADLAYILSMPCGCHLIINNPNFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRSSPHFVEVKGDLTAKXWVLLALLEARQDHGALDCCVVVILSHGQ 240
DB 181 TGSNIDCEKLRRLRRSSPHFVEVKGDLTAKXWVLLALLEARQDHGALDCCVVVILSHGQ 240
QY 241 ASHLQFPGAVGTDCPVSVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
DB 241 ASHLQFPGAVGTDCPVSVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
QY 301 TSPEDSPGNSPEPDATPFQGLRTFDQLDAISSLPTSPDIFVSYSTPFGFVSWDRPKSG 360
DB 301 TSPEDSPGNSPEPDATPFQGLRTFDQLDAISSLPTSPDIFVSYSTPFGFVSWDRPKSG 360
QY 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLFKTS 416
DB 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLFKTS 416

RESULT 8
US-09-311-760-2
; Sequence 2, Application US/09311760
; Patent No. 6274318
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/311,760
; FILING DATE: 13-May-1999
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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/865,579
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-311-760-2

Query Match          98.8%; Score 2153; DB 3; Length 416;
Best Local Similarity 98.8%; Pred. No. 4.8e-227;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRRCLRLVEELQVDOLWDVLLSRELFRPHMIEDIORAGSGSRDQAROLII 60
DB 1 MDEADRLRLRRCLRLVEELQVDOLWDVLLSRELFRPHMIEDIORAGSGSRDQAROLII 60
QY 61 DLETRGQALPLFTSCLEDTGQDMLASFLRTRNQAGKLSKPTLENLTPVVLRLPEIRKEV 120
DB 61 DLETRGQALPLFTSCLEDTGQDMLASFLRTRNQAGKLSKPTLENLTPVVLRLPEIRKEV 120
QY 121 LRPEPRPVDIGSGGFDGVALESRLGNADLAYILSMPECHGLIINNVPFCRESGLRTR 180
DB 121 LRPEPRPVDIGSGGFDGVALESRLGNADLAYILSMPECHGLIINNVPFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRFSSLHFMVVEVKGDLTAKWVLALLELARQDHGALDCCVVVTLSHGCQ 240
DB 181 TGSNIDCEKLRRLRRFSSLHFMVVEVKGDLTAKWVLALLELARQDHGALDCCVVVTLSHGCQ 240
QY 241 ASHLQPPGAVYGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIACGGQKDHGFVEAS 300
DB 241 ASHLQPPGAVYGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIACGGQKDHGFVEAS 300
QY 301 TSPEDSPGNSNPEDATPFOEGLRTFDQLDAISLTPSPDIFVSYSTFPFGVSWRDPKSG 360
DB 301 TSPEDSPGNSNPEDATPFOEGLRTFDQLDAISLTPSPDIFVSYSTFPFGVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
DB 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 9
US-08-865-579-2
; Sequence 2, Application US/08865579
; Patent No. 6455296
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-865-579-2

Query Match          98.8%; Score 2153; DB 4; Length 416;
Best Local Similarity 98.8%; Pred. No. 4.8e-227;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRRCLRLVEELQVDOLWDVLLSRELFRPHMIEDIORAGSGSRDQAROLII 60
DB 1 MDEADRLRLRRCLRLVEELQVDOLWDVLLSRELFRPHMIEDIORAGSGSRDQAROLII 60
QY 61 DLETRGQALPLFTSCLEDTGQDMLASFLRTRNQAGKLSKPTLENLTPVVLRLPEIRKEV 120
DB 61 DLETRGQALPLFTSCLEDTGQDMLASFLRTRNQAGKLSKPTLENLTPVVLRLPEIRKEV 120
QY 121 LRPEPRPVDIGSGGFDGVALESRLGNADLAYILSMPECHGLIINNVPFCRESGLRTR 180
DB 121 LRPEPRPVDIGSGGFDGVALESRLGNADLAYILSMPECHGLIINNVPFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRFSSLHFMVVEVKGDLTAKWVLALLELARQDHGALDCCVVVTLSHGCQ 240
DB 181 TGSNIDCEKLRRLRRFSSLHFMVVEVKGDLTAKWVLALLELARQDHGALDCCVVVTLSHGCQ 240
QY 241 ASHLQPPGAVYGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIACGGQKDHGFVEAS 300
DB 241 ASHLQPPGAVYGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIACGGQKDHGFVEAS 300
QY 301 TSPEDSPGNSNPEDATPFOEGLRTFDQLDAISLTPSPDIFVSYSTFPFGVSWRDPKSG 360
DB 301 TSPEDSPGNSNPEDATPFOEGLRTFDQLDAISLTPSPDIFVSYSTFPFGVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
DB 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 10
US-10-059-749-2
; Sequence 2, Application US/10059749
; Patent No. 6566505
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

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; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,308
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: NORTH, ROBERT J
; REGISTRATION NUMBER: 27,366
; REFERENCE/DOCKET NUMBER: 19840 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-7262
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-964-308-6

Query Match 19.2%; Score 418; DB 3; Length 277;
Best Local Similarity 33.2%; Pred. No. 3.6e-37;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAYILSMPCGCHCLIIINNVCRESGLRTRTGSNIDCEKLRFRSSLHFMVVEVKGDLTA 209
DB 34 DNSYMDYPMGLCIIINNKNFHKTGTSRSGTDVDAANLRETRPNLKYEVRNKNDLTR 93
QY 210 KMWLALALELARQDHGALDCCVWVILSHGCOASHLQFPFVAVYGTDCGCVSVVEKIVNIFNG 269
DB 94 BEIVELMRDVSKEDHSKSSFVCVLLSHGEE-----GIIFGTNG-PVDLKKIINFPRG 145
QY 270 TSCPSLGGKPKLFFITQACGGQKHGFEVASTSPEDSPGSGNPEPDATPFQEGLETFDQL 329
DB 146 DRCRSLTGKPKLFIITQACRGTGLDCGIETDSGVDDM----- 182
QY 330 DAISLPTPSDFVSYSTFPFVSWRDPKSGSWYVETLDDIFEOWAHSEDLQSLLRVAN 389
DB 183 -ACHKIPVEADFLYASTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFPHILTRVNR 241
QY 390 AVSVK-----GIYKQMPGCFNFKLFF 413
DB 242 KVATEFESFSDATFHAKKQIPCIIVSMLTKELYF 275

Search completed: August 3, 2004, 08:55:37
Job time : 20 secs
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RESULT 15
US-08-462-969B-4
; Sequence 4, Application US/08462969B
; Patent No. 6087150
; GENERAL INFORMATION:
; APPLICANT: He, Wei-Wu et al.
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
; TITLE OF INVENTION: Like Apoptosis Protease 3 and 4
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 08:59:31 ; Search time 16 Seconds
(without alignments)
2500.980 Million cell updates/sec

Title: US-09-961-201a-1

Perfect score: 2180

Sequence: 1 MDEADRLRLRCRLRLVEEL.....YKQMPGCFNLEKLLFFKTS 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 208102

Minimum DB seq length: 0

Maximum DB seq length: 416

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2180	100.0	416	2 G02635	ICE-LAP6 - human
2	429	19.7	277	2 S64710	cysteine proteinas
3	418	19.2	277	2 A55315	cysteine proteinas
4	408	18.7	277	2 JC5410	CPP32 protein - mo
5	384	17.6	212	2 I67437	cysteine proteinas
6	304	13.9	312	2 B54821	apoptosis regulato
7	268.5	12.3	402	2 A46495	IL-1 beta converta
8	262	12.0	182	2 I67436	interleukin-1-beta
9	259	11.9	404	2 A42677	interleukin-1-beta
10	256.5	11.8	383	2 A56084	interleukin-1-beta
11	239.5	11.0	242	2 JC7517	caspase-14/a - hum
12	220	10.1	311	2 B56084	interleukin-1-beta
13	209	9.6	377	2 A57511	interleukin-1-beta
14	186	8.5	263	2 C56084	interleukin-1-beta
15	154.5	7.1	149	2 T43637	interleukin-1-beta
16	151.5	6.9	136	2 I53300	caspase protein 1C
17	115.5	5.3	394	2 T26968	interleukin-1-beta
18	107.5	4.9	139	2 T43642	hypothetical prote
19	96.5	4.4	369	2 T32781	caspase protein 3
20	91.5	4.2	376	2 JC7759	hypothetical prote
21	89.5	4.1	395	2 T05906	alcohol dehydrogen
22	89	4.1	369	2 T20505	probable polygalac
23	85.5	3.9	273	2 D84195	hypothetical prote
24	84.5	3.9	311	2 D75405	oxidoreductase [im
25	84.5	3.9	317	2 A59292	conserved hypothet
26	84	3.9	276	2 AE0485	probable type II m
27	83	3.8	351	2 T25448	conserved hypothet
28	83	3.8	364	2 F83278	hypothetical prote
29	81.5	3.7	210	2 AG0534	phospho-2-dehydro-
					hypothetical prote

30 81 3.7 163 1 JQ0144 probable protein-d
31 81 3.7 163 2 F82988 disulfide bond for
32 80.5 3.7 345 2 JQ0429 hypothetical 37.1k
33 80.5 3.7 361 2 T38693 probable trna prot
34 80 3.7 288 2 A87051 probable protopor
35 80 3.7 375 2 T48807 hypothetical prote
36 79.5 3.6 195 2 S28739 hypothetical prote
37 79.5 3.6 284 2 G87701 acyl-CoA thioester
38 79.5 3.6 375 1 S62638 alcohol dehydrogen
39 79.5 3.6 381 2 G96804 hypothetical prote
40 79 3.6 191 2 T09985 protoporphyrinogen
41 79 3.6 398 2 H81090 acetylorithine am
42 78.5 3.6 328 2 S35336 transcription fact
43 78.5 3.6 350 1 ADECHF 2-dehydro-3-deoxy-
44 78.5 3.6 350 2 F90726 2-dehydro-3-deoxy-
45 78.5 3.6 350 2 G85577 2-dehydro-3-deoxy-

ALIGNMENTS

RESULT 1

G02635

ICE-LAP6 - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999

C:Accession: G02635

R:Duan, H.; Orth, K.; Chinnaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.; Dixit, V.

submitted to the EMBL Data Library, April 1996

A:Reference number: H01513

A:Accession: G02635

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-416 <DUA>

A:Cross-references: EMBL:U56390; NID:gl336026; PIDN:AAC50640.1; PID:gl336027

Query Match

Best Local Similarity 100.0%; Score 2180; DB 2; Length 416;

Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Qy 61 DLETRGSOALPLFTSCLEDTGQDMLASFLRTNQAGKLSKPTLENLTPVVLREIRKPEV 120
Db 61 DLETRGSOALPLFTSCLEDTGQDMLASFLRTNQAGKLSKPTLENLTPVVLREIRKPEV 120
Qy 121 LRPEPRPVDIGSGFGDVGALSLRGADLAVILSMPCGHCLIIINNVPFRESGLRTR 180
Db 121 LRPEPRPVDIGSGFGDVGALSLRGADLAVILSMPCGHCLIIINNVPFRESGLRTR 180
Qy 181 TGSNIDCEKLRFRFSSLFHFMVEVKGDLTAKKMWLALLELARQDHGALDCCVWLSHGCO 240
Db 181 TGSNIDCEKLRFRFSSLFHFMVEVKGDLTAKKMWLALLELARQDHGALDCCVWLSHGCO 240
Qy 241 ASHLQPFAGVYGTGCPVSVEKIVNFNGTSCPSLGGKPKLFTFIQACGGKQDHGEVAS 300
Db 241 ASHLQPFAGVYGTGCPVSVEKIVNFNGTSCPSLGGKPKLFTFIQACGGKQDHGEVAS 300
Qy 301 TSPEDSPGSNPEPDATPFQEGRLTFDQLDAISSLTPSDIFVSYSTFFGFSWRDPKSG 360
Db 301 TSPEDSPGSNPEPDATPFQEGRLTFDQLDAISSLTPSDIFVSYSTFFGFSWRDPKSG 360
Qy 361 SWYVETLDDIFQWAHSEDLQSLILRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
Db 361 SWYVETLDDIFQWAHSEDLQSLILRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416

RESULT 2

S64710

cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster

C:Species: Cricetulus griseus (Chinese hamster)

C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C/Accession: S64710; S72395
R/Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.
EMBO J. 15, 1012-1020, 1996
A/Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during
A/Reference number: S64710; MUID:96183185; PMID:8605870
A/Accession: S64710
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-277 <WAN>
A/Cross-references: EMBL:U27463
R/Wang, X.
submitted to the EMBL Data Library, May 1995
A/Reference number: S72395
A/Accession: S72395
A/Molecule type: mRNA
A/Residues: 1-79, 'A', 81-146, 'Y', 148-277 <WAW>
A/Cross-references: EMBL:U27463; NID:g1244443; PIDN:AA801511.1; PID:g1244444
C/Keywords: apoptosis; cvstaine proteinase; hydrolase

[illegible]

RESULT 3

A55315

cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human

N/Alternate names: cysteine proteinase CPP32

C/Species: Homo sapiens (man)

C/Date: 06-Feb-1995 #sequence revision 06-Feb-1995 #text_change 01-Dec-2000

C/Accession: A55315; S58899; I39005

R/Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.

J. Biol. Chem. 269, 30761-30764, 1994

A/Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans

A/Reference number: A55315; MUID:95074098; PMID:7983002

A/Accession: A55315

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-277 <PER>

A/Cross-references: GB:U13737; NID:G561665; PIDN:AAA65015.1; PID:G561666

R/Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant, M.;

Yu, V.L.; Miller, D.K.

Nature 376, 37-43, 1995

A/Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalian

A/Reference number: S58899; MUID:95319529; PMID:7596430

A/Accession: S58899

A/Molecule type: protein

A/Residues: 29-46;176-189, E',191-193 <NIC>

R/Tewari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poirier,

Cell 81, 801-809, 1995

A/Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease

A/Reference number: A56324; MUID:95292347; PMID:7774019

```

A;Accession: I39005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-189, 'E', /191-277 <RES>
A;Cross-references: EMBL:U26943; NID:G857568; PIDN:AAA74929.1; PID:G857569
C;Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

      Query Match      19.2%; Score 418; DB 2; Length 277;
      Best Local Similarity 33.2%; Pred. No. 4.5e-28;
      Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 34;

QY      150 DLAIIISMPCGCLIIINNVCRESGLTRTGSNIDCEKLRERFSSLHFMVEVKGDLTA 209
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      34 DNSYKMDYPMGLCIIIINNKNFKHKTGMTSRSGTDVDAANLRETFRLNKYEVRKNKDLTR 93
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      210 KKVALLLELARQDHGALDCVVVILSHGCGQASHLPFGAVYGTGDCPVSVEKIVNIFNG 269
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      94 EEIVELMRDYSKEDHSKRSSFVCLVLSHGEE-----GIIFGFG-PVDLKITNFRG 145
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      270 TSPSLGGKPKLFFIQACGGEQKHGFVASTSPEDSPGSNPEDATPFQEGRLTFDQL 329
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      146 DRCSLTGKPKLFIIQCRTELDGLETDSGVDDM----- 182
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      330 DAISSLPTSDIIFVSYTFPGFVSWRDPKSGSWYVETLDDIFQWHAHSDLOQLLLRYAN 389
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      183 -ACHKIPVDAFLYAYSTAGYYSWRNSKGSNFIQSLCAMLKQYADLFMFHILTRVNR 241
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      390 AVSVK-----GIYKQMPGCFNLRKKLFF 413
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      242 KYAIFERSFSDATFHAKKOIPCTVSMILTKELYF 275
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 4

JC5410

Cp32 protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999

C:Accession: JC5410

R:Mukasa, I.; Urabe, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.

Biochem. Biophys. Res. Commun. 234, 770-774, 1997

A:Title: Specific expression of Cp32 in sensory neurons of mouse embryos and

A:Reference number: JC5410; MUID:97224429; PMID:9070890

A:Accession: JC5410

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-277 <MUK>

A:Cross-references: DDBJ:D86352

A:Experimental source: embryo

C:Comment: This protein is involved in the apoptosis of dorsal root ganglia ne

Query Match	18.7%	Score 408;	DB 2;	Length 277;	
Best local Similarity	32.1%	Pred. NO. 3.2e-27;			
Matches	88;	Conservative 52;	Mismatches -9;	Indels 42;	Gaps 4
QY	150	DLAYILSMPEPGCHCLIIINNVPFCRESGLRTRTGSNIDCEKLLRRFSSLHFVWVVKDGLTA	209		
DB	34	DSSYKWDYPWEMGICIIITKNKFNHKSSTGMSRSSGTVDAAANLRETEMGLKYEVRNKNDLTR	93		
QY	210	KKKVALLLELARQDHGALDCVVILSHGCCASHLQFPQAVYGTGCPVSVKEKVIENIENG	269		
DB	94	BEIMLMDVSXKEDHSKSSFFVCVILSHGDE-----GVIFGNG-PVDLKKLTSFPG	145		
QY	270	TSCPSLGGKPKLFFHQACGGEGOKHGFVASTSPEDSGSPGNPEPDATFOEGLRTFPOL	329		
DB	146	DYCRSLTKPKLFIQACRGTELDCCGIETSDGTDEEM-----	182		
QY	330	DAISLSPEDSIFVSYPFPGVSRWRDPKSGSWYVETLDDIFQWHAHSEDLOSLLLRVAN	389		
DB	183	-ACQKIPVEADFLYAYSTAPGYISWRNSKGSWFIQSLCSMLKLYAHKLEFMHILTRVR	241		
QY	390	AVSVK-----GIYKQMPGCGFNIRKKLFF	413		
DB	242	KVATFESFSLDSTPHAKKQIPICVISMULTKELYF	275		


```
QY 213 VLALLEAR-QDHGALDCCVVVILSHGQASHLQPGAVYGTDCGPV-SVEKIVNIENG 270
Db 211 VKEVKEFAACEPHKTSDBSTFLVFMHSHGIQEG---ICGTTYGNEVSDILKVDTFIQMMNTL 267
QY 271 SCPSLGGKPKLFFFTQACCGEOKDHGFEVASTSPDESFGSNPEPDATPFQGLRT--FD 327
Db 268 KCPSLKDKPKVILIIQACGKQ--GVVLLKDSVRDS-----EDFLTDALFE 312
QY 328 QLDAISSLPTSDIFVSYSTPFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLRV 387
Db 313 D-DGIKKAHIEKDFIAFCSTPDNVSWRHPVRSGLFIESLIKHMKEYAMSCDLEDFPKV 371
QY 388 ANAVSVKGIYKQPCFNLKRLPF 413
Db 372 RFSFQEPFRLQMPADRVTLLTKREY 397

RESULT 8
I67436
interleukin-1-beta-converting enzyme and ced-3 homolog-1, long isoform - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: I67436
R:Flaws, J.A.; Kugy, K.; Trbovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirshfield, A.N.; Til
Endocrinology 136, 5042-5053, 1995
A:Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel
nuloa cells of the ovarian follicle.
A:Reference number: I53300; MUID:96042508; PMID:7588240
A:Accession: I67436
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-182 <RES>
A:Cross-references: EMBL:U34684; NID:g1004368; PIDN:AAC52260.1; PID:g1004369

Query Match 12.0%; Score 262; DB 2; Length 182;
Best Local Similarity 33.3%; Pred. No. 5.9e-15;
Matches 63; Conservative 33; Mismatches 75; Indels 18; Gaps 4;
QY 159 PGGHCLIIINNFCRESGLRTTGSNIDCEKLRFPSSLHFVVEVKGDLTAKKVVALLLE 218
Db 1 PRGLALVMSNVHFTGKDLFRSGVDVHTTLVTLFKLLGVNVHVLVDQTAQEMOEKLN 60
QY 219 IAR-QDHGALDCCVVVILSHGQASHLQPGAVYGTDCGPVSEKIVNIFNGTSCPSLGG 277
Db 61 FAQLPAHRVTDSCVALLSHGVE-----GGYIGVDGKLLQQLQEVRLFDNANCSLQN 113
QY 278 KPCLFTIQCGGQKDHGFEVASTSPDESFGSNPEPDATPFQGLRTFDQLDAISSLPT 337
Db 114 KPMVFIQACRGDETGRGVDDQDGKNHAQPPGC--EESDTVKEELMK-----MRLPT 163
QY 338 PSDIFVSYS 346
Db 164 RSDMICVYA 172

RESULT 9
A42677
interleukin-1 beta converting enzyme (EC 3.4.22.-) - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: A54263; A42677; S21734; S24164
R:Gerrett, D.P.; Hollingsworth, L.T.; Kozlosky, C.J.; Valentine, M.B.; Shapiro, D.N.; M
Genomics 20, 469-473, 1994
A:Title: Molecular characterization of the gene for human interleukin-1beta converting e
A:Reference number: A54263; MUID:94307734; PMID:8034320
A:Accession: A54263
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-404 <CE2>
A:Cross-references: GB:L27475
R:Gerrett, D.P.; Kozlosky, C.J.; Mosley, B.; Nelson, N.; Van Ness, K.; Greenstreet, T.A
Science 256, 97-100, 1992
A:Title: Molecular cloning of the interleukin-1beta converting enzyme.
```

```
A:Reference number: A42677; MUID:92229430; PMID:1373520
A:Accession: A42677
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-404 <CER>
A:Cross-references: GB:M87507; NID:9435598; PIDN:AAA66942.1; PID:g186286
R:Thornberry, N.A.; Bull, H.G.; Calaycay, J.R.; Chapman, K.T.; Howard, A.D.; Kostura, M.;
J.; Ding, G.J.F.; Egger, L.A.; Gaffney, E.P.; Lamjuco, G.; Palyha, O.C.; Raju, S.M.; Rol
cci, M.J.
Nature 356, 768-774, 1992
A:Title: A novel heterodimeric cysteine protease is required for interleukin-1beta proce
A:Reference number: S21734; MUID:92244338; PMID:1574116
A:Accession: S21734
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-404 <THO>
A:Cross-references: EMBL:X65019; NID:933792; PIDN:CAA6153.1; PID:g933793
R:Kronheim, S.R.; Muma, A.; Greenstreet, T.; Glackin, P.J.; van Ness, K.; March, C.J.;
Arch. Biochem. Biophys. 296, 698-703, 1992
A:Title: Purification of interleukin-1beta converting enzyme, the protease that cleaves
A:Reference number: S24164; MUID:92337439; PMID:1321594
A:Accession: S24164
A:Status: preliminary
A:Molecule type: protein
A:Residues: 120-135,'AX',138-139,'X',141-142 <KRO>
C:Genetics:
A:Gene: GDB:ILLIBC
A:Cross-references: GDB:132368; OMIM:147678
A:Map position: 11q23-11q23
C:Keywords: cysteine proteinase; hydrolase

Query Match 11.9%; Score 259; DB 2; Length 404;
Best Local Similarity 24.3%; Pred. No. 3.1e-14;
Matches 104; Conservative 62; Mismatches 176; Indels 86; Gaps 14;
QY 10 RRCRLRVEELQVDQLWDVLLSRELFRPHMIEDIORAGSGSRDQARQLIIDLETRGSA 69
Db 10 RKLFRSNGEGTINGLLDELQTRVLNKEEMKVKRE-NATVMDKTRALIDSVIPKGAQA 68
QY 70 LPLFTS--CLEP-----TGQDLASFRTNRQAGLSKPTLENLTFVVLRLPEIRKP 118
Db 69 COICITYICEEDSYLAGTLGJSADQTSNYLNNQSQGVLS-----SFPAP 114
QY 119 EYLRPETPRVDIGSGGFDVGALRESL-----RGNADLAYILSMBPCH-CLIIINNVP 172
Db 115 QAVQNPAPTSSSGEGNVKLSLEAQRIWKQSAEIVPIMDKSRTLALICNEEF- 173
QY 173 RESGLRTRTGSNIDCEKLRFPSSLHFVVEVKGDLTAKKVVALLLELA-RQDHGALDCCV 231
Db 174 --DSIPRRTGAEVDITGMTLLQLNLGYSVDVKKNLTASDMTTELEFAHRPEKTSSTF 231
QY 232 VVILSHG-----CQASHL-QFFGAVYGTDCGPVSEKIVNIFNGTSCPSLGGKPKLFFIQ 285
Db 232 LVFMHSHGIREG:CGKKHSEQVPDI-----LQNLAI FNMNLNTKNCPSLKDKPKVILIIQ 283
QY 286 ACGEQKDHGFEVASTSPDESFP-----GSNPEPDATPFQGLRTFDQLDAIS 333
Db 284 ACRG-----DSFGVVWFKDSVGSVGNLSLPTTEEFED-----DAIK 319
QY 334 SLPTPSDIFVSYSTPFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLRVANVSV 393
Db 320 KAHIEKDFIAFCSTPDNVSWRHPRTMGVSFVIGRLIEHMQEYACSCDVERIFRKVRFSFQ 379
QY 394 KGIYKOMP 401
Db 380 PDGRAOMP 387

RESULT 10
A56084
interleukin-1beta converting enzyme beta isozyme - human
C:Species: Homo sapiens (man)
C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
```

C;Accession: A56084
E;Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
J. Biol. Chem. 270, 4312-4317, 1995

A;Title: Cloning and expression of four novel isoforms of human interleukin-beta converting enzyme.

A;Reference number: A56084; MUID:95181414; PMID:7876192

A;Accession: A56084

A>Status: preliminary

A:Molecule type: mRNA

A;Residues: 1-383 <ALN>

A;Cross-references: GB:U13697; NID:g717039; PIDN:AAC50107.1; PID:g717040

C;Genetics:

A;Gene: IL1BCE

C;Keywords: alternative splicing

Query Match 11.8%; Score 256.5; DB 2; Length 383;
Best Local Similarity 25.1%; Pred.No. 4.8e-14;
Matches 105; Conservative 60; Mismatches 165; Indels 89; Gaps 15;

QY 10 RRCLRLVLEQLVDQLMDVLILLSRELPRPHMEDIQAGSGRRDQAQRLLDLLETGSOA 69
| : : : : :
Db 10 RKLFIKSMGEQTGLLDELLOTRVLNKKEEKVKRE-NATVMDKTRALIDSVIPKAQA 68
| : : : : :
QY 70 LPIFIS--CLEDTQQDMLASFLRTNRQAKLSKPTLENLTFFVILRPEIRKPEVLRPETP 127
| : : | : : |||||
Db 69 CQCITCYICBED-----SYL-----AGTLGLSA-----APQAVQNPMAM 102
| : : : : :
QY 128 PVDIGSGGGFDVGALESL-----RGNAADLAYILSMPCGH-CLIIINNVNFCRESGRTRT 181
| : : : : :
Db 103 PTSSGSEGVNLCSLEEAIWIWQKGAEIYIPIMDKSRTRLALIICNEEF---DSIPRRT 159
| : : : : :
QY 182 GSNIDCEKLRFRSLLHFMYVEKGDLTAKKWLALLLELA-RQDHGALDCCVVVILSHG-- 238
| : : : : :
Db 160 GAENVDTGTMTLLQLNGYSVDVKKNLTASDMTTTEAFARPEHKTSDSFTLVFMHGIR 219
| : : : : :
QY 239 ---COASHL-QFPNAVYGTCGPVSVEKIWNIENTSCPSLGKPPLFTIQCAGGEOKDH 294
| : : : : :
Db 220 EGICGKHHEQVPDI-----LQNALTFNMINTKNCPSLKDPKVLI IQACRG---- 266
| : : : : :
QY 295 GFEEASTSPDESP-----GSNPEDPATPFQEGLRTFDQLDAISSLPSPDIF 342
| : : : : :
Db 267 -----DSPGVVWFKDSDVSVGNLSLPTTERFED-----DAIKAAHIEKDFI 307
| : : : : :
QY 343 VSYSTPPGFVSWDRPKSGSHYYVTLDIDEFWAHNSDLQSLLLVRVANVSKGIYKMP 401
| : : | : : |||||
Db 308 AFCSTTPDNWSRHPTMGVFICGLRIEHMQEYACSDVEEIFRKRVFSFEQPDPGRAMP 366
| : : : : :

RESULT 11
JC7517

C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C;Accession: JC7517

R;Ackhart, L.; Ban, J.; Fischer, H.; Tschachler, E.
Biochem. Biophys. Res. Commun. 277, 655-659, 2000

A;Title: Caspase-14: Analysis of gene structure and mRNA expression during keratinocyte differentiation.

A;Reference number: JC7517; MUID:20517231; PMID:11062009

A;Contents: Epidermal keratinocytes

A;Accession: JC7517

A:Molecule type: mRNA

A;Residues: 1-242 <ECK>

A;Cross-references: GB:AF097874

C;Comment: This enzyme accumulates during keratinocyte differentiation and is activated by TNF-alpha.

A;Gene: casp-14/a

A;Map position: 19p13.1

A;Introns: 9/3; 59/3; 135/1; 174/1; 208/3

C;Keywords: differentiation

```

Qy 178 RTRGTSNTDCEKLRRRFSSILHFVMEVVKGDLTAKXKMLALLEL-----ARQDHGALDCCVV 232
Db 27 KAREGESDLDALHEMFQRLRFESTMTKRDPTAEQFOBELEKFOQAIDRED--PVSCAFV 84
Qy 233 VILSHGCCAASHLQFPQVAVYGTDCPVSVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEOK 292
Db 85 VIMAHGR-----GFLKGEDGEMVKLENLEFALNNKCOALRAKPKVVIIOCRGEOR 137
Qy 293 DHGFEVASTPDESPGSGNPEPDATPFQGLRTFDQL-----DAISSLTPSDIFVSYST 347
Db 138 DPQ-----ETVGG-----DEIVMWIKDSPQTIPTYTDALHYST 171
Qy 348 PPGFVSWRDPKSGSWYVETLDDIF-EQWAH-SEDLOSLLLRVANAVSVK--GIYKQMPGC 403
Db 172 VEGIAYXHDQKSGCFIQTLVDVFTKRGHILELLEVTERRMAEELVQEGKARKTNPEI 231
Qy 404 FNFLRKKLFFK 414
Db 232 QSTLRKRLYLQ 242

RESULT 12
B56084
interleukin-1beta converting enzyme gamma isozyme - human
C:Species: Homo sapiens (man)
C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
C:Accession: B56084
R:Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
J. Biol. Chem. 270, 4312-4317, 1995
A:Title: Cloning and expression of four novel isoforms of human interleukin-1beta conver
A:Reference number: A56084; MUID:95181414; PMID:7876192
A:Accession: B56084
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-311 <ALN>
A:Cross-references: GB:U13698; NID:g717041; PIDN:AAC50108.1; PID:g717042
C:Gene: IL1BCE
C:Keywords: alternative splicing

Query Match 10.1%; Score 220; DB 2; Length 311;
Best Local Similarity 24.9%; Pred. No. 4.8e-11;
Matches 82; Conservative 47; Mismatches 140; Indels 60; Gaps 10;

Qy 98 LSKETLENLPVVLRPETRKPEVLRPETPRVDIIGSGGPDVGALES-----RGNADLA 152
Db 1 MADKVLREKRLKFLIRSMGEAPQAVQNDPAMPTSSGSEGNVKLCSLEEAQRIMKQKSAEY 60
Qy 153 YILSMPECGH-CLIIINVNFCSRESGLRTRTGSNIDCEKLRFRFSSILHFVMEVVKGDLTAKK 211
Db 61 PIMDKSRTRLALIIICNEEF--DSIPRTGAEVITGMTLLQNLGYSVDVKNNLTASD 117
Qy 212 MVIALLELA-RQDHGALDCCVVWILSHG-----COASHL-QPPGAVYGTDCPVSVEKIV 264
Db 118 MTTELEFAHRPEKTSDDSTFLVMSHGIREGICGKHSEQVPDI-----LQNAIF 169
Qy 265 NIENGTSCLPSLGGKPKLFFIOACGGEQKHGFVASTSPEDESP-----GSPN 312
Db 170 NMLTNKCPSLKDKPKVILIIQACRG-----DSPGVVWFKDSVGVSGNLS 213
Qy 313 EPDATPFQEGRLTDPQLDIAISSLTPSDIFVSYSTFPFGVSWRDPKSGSWYVETLDDIPE 372
Db 214 LPITTEEFED-----DAIKKAHEKDFIAFCSTPDNVSWRHHFTMGSVFICRLIEHMQ 265
Qy 373 QWAHSEDLOSLLLRVANAVSVKGIYKQMP 401
Db 266 EVACSDVEIFRKVRFSFEOPDGRAOWP 294

```

Query Match	11.0%;	Score 239.5;	DB 2;	Length 242;
Best Local Similarity	28.7%;	Pred. No. 7.3e-13;		
Matches	72;	Conservative 46;	Mismatches 84;	Indels 49;
			Gaps 9;	Gaps 9;

RESULT 13
A57511
interleukin-1 beta converting enzyme (EC 3.4.22.-) ICErel-II - human
N;Alternate names: protease TX

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OM protein - protein search, using sw model

Run on: August 3, 2004, 08:55:41 ; Search time 13 Seconds
(without alignments)
1666.245 Million cell updates/sec

Title: US-09-961-201a-1

Perfect score: 2180

Sequence: 1 MDEADRLRLRCRLRLVBE.....YKQMPGCFNLRKKLFFKTS 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 98277

Minimum DB seq length: 0

Maximum DB seq length: 416

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2166	99.4	416	1	ICE9 HUMAN
2	428	19.6	277	1	ICE3_XENLA
3	418	19.2	277	1	ICE3_HUMAN
4	409	19.2	277	1	ICE3_MOUSE
5	364.5	16.7	303	1	ICE3_RAT
6	364.5	16.7	303	1	ICE7_MESAU
7	361.5	16.6	303	1	ICE7_HUMAN
8	350.5	16.1	303	1	ICE7_MOUSE
9	349	16.0	282	1	ICE3_XENLA
10	334	14.9	339	1	ICE_MOUSE
11	322	14.8	276	1	ICE_MOUSE
12	320	14.7	323	1	ICE1_DROME
13	312.5	14.3	312	1	ICE2_RAT
14	311.5	14.3	293	1	ICE6_HUMAN
15	300.5	13.8	405	1	ILBC_HORSE
16	297.5	13.6	299	1	ICE1_SPOFR
17	279	12.8	382	1	ICEB_XENLA
18	278	12.8	404	1	ILBC_PIG
19	274	12.6	410	1	ILBC_FELCA
20	270.5	12.4	402	1	ILBC_RAT
21	268.5	12.3	402	1	ILBC_MOUSE
22	262	12.0	404	1	ILBC_CANFA
23	259	11.9	404	1	ILBC_HUMAN
24	256	11.7	386	1	ICEA_XENLA
25	253	11.6	257	1	ICEE_MOUSE
26	239.5	11.0	242	1	ICEE_HUMAN
27	232	10.6	377	1	ICED_BOVIN
28	212	9.7	373	1	ICE4_MOUSE
29	209	9.6	377	1	ICE4_HUMAN
30	97.5	4.5	382	1	AMAC_HUMAN
31	83.5	3.8	199	1	CRAD_MOUSE
32	83.5	3.8	410	1	AUP1_MOUSE
33	81	3.7	163	1	DSB1_PSEAE

34	81	3.7	371	1	PGLR_PENJA	O42824 penicillium
35	80.5	3.7	345	1	YT37_STRFR	P20187 streptomyce
36	80.5	3.7	375	1	ADHH_GADMO	P81600 gadus morhu
37	80	3.7	288	1	HEMK_MYCLE	P45832 mycobacteri
38	80	3.7	291	1	EPG_PROMM	Q7V8Y5 prochloroco
39	79.5	3.6	375	1	ADHA_UROHA	P25405 uromastys h
40	79	3.6	398	1	ARGD_NEIMB	Q9JY44 neisseria m
41	78.5	3.6	290	1	SYGA_FUSNN	Q8th45 fusobacteri
42	78.5	3.6	328	1	CEBB_CHICK	Q05826 gallus gall
43	78.5	3.6	350	1	AROG_ECOLI	P00886 escherichia
44	78.5	3.6	363	1	GCST_HALNI	Q9npj7 halobacteri
45	78	3.6	199	1	CRAD_HUMAN	P78560 homo sapien

ALIGNMENTS

RESULT 1

ICE9 HUMAN

ID ICE9 HUMAN STANDARD; PRT; 416 AA.

AC P55211; Q95348; Q92852; Q9BQ62; Q9UEQ3; Q9UIJ8;

DT 01-OCT-1996 (Rel. 34, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Caspase-9 precursor (EC 3.4.22.-) (CASP-9) (ICE-like apoptotic

DE protease 6) (ICE-LAP6) (Apoptotic protease Mch-6) (Apoptotic protease

DE activating factor 3) (APAF-3).

GN CASP9 OR MCH6.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP MEDLINE=96279246; PubMed=8663294;

RA Duan H., Orth K., Chinnaiyan A.M., Poirier G.G., Froelich C.J.,

RA He W.-W., Dixit V.M.;

RT "ICE-LAP6, a novel member of the ICE/Ced-3 gene family, is activated

RT by the cytotoxic T cell protease granzyme B.;"

RL J. Biol. Chem. 271:16720-16724(1996).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1), AND PROCESSING.

RC TISSUE=T-cell;

RA MEDLINE=97059171; PubMed=8900201;

RA Srinivasula S.M., Fernandes-Alnemri T., Zangrilli J., Robertson N.,

RA Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,

RA Alnemri E.S.;

RT "The Ced-3/interleukin 1beta converting enzyme-like homolog Mch6 and

RT the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic

RT mediator CPP32.;"

RL J. Biol. Chem. 271:27099-27106(1996).

RN [3]

RP SEQUENCE FROM N.A.

RA MEDLINE=99315341; PubMed=10384055;

RA Hadano S., Nasir J., Nichol K., Rasper D.M., Vaillancourt J.P.,;

RA Sherer S.W., Beatty B.G., Ikeda J.E., Nicholson D.W., Hayden M.R.;

RT "Genomic organization of the human caspase-9 gene on chromosome

RT 1p36.1-p36.3.;"

RL Mamm. Genome 10:757-760(1999).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RA MEDLINE=99168502; PubMed=10070954;

RA Srinivasula S.M., Ahmad M., Guo Y., Zhan Y., Lazebnik Y.,

RA Fernandes-Alnemri T., Alnemri E.S.;

RT "Identification of an endogenous dominant-negative short isoform of

RT caspase-9 that can regulate apoptosis.;"

RL Cancer Res. 59:999-1002(1999).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RA TISSUE=Stomach cancer;

RA Izawa M., Mori T., Ito H., Saitenji T.;

RT "Molecular cloning and sequencing of a cDNA predicting an alternative

RT form of pro-caspase-9 from human gastric cancer cell lines.;"


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Query Match 99.4%; Score 2166; DB 1; Length 416;
Best Local Similarity 99.3%; Pred. No. 8.4e-177;
Matches 413; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDEADRLRLCRRLVEELQVDLMDVLLSRELFRPHMIEDIORAGSGSRDDAROLII 60
DB 1 MDEADRLRLCRRLVEELQVDLMDVLLSRELFRPHMIEDIORAGSGSRDDAROLII 60
QY 61 DLETGSGALPLFISCLDGTGDMLASFLRNQAGKLSKPTLENLTPVILRPEIRKPEV 120
DB 61 DLETGSGALPLFISCLDGTGDMLASFLRNQAGKLSKPTLENLTPVILRPEIRKPEV 120
QY 121 LRPETPRVDTCGSGFGDVGALSLRGNADLAILSMPECGHCLIIINNVPFCRESGLRTR 180
DB 121 LRPETPRVDTCGSGFGDVGALSLRGNADLAILSMPECGHCLIIINNVPFCRESGLRTR 180
QY 181 TGSNIDCEKLRFRFSLHFMVEVKGLTAKKMWLALLLALRODHGALDCCVVVILSHGCQ 240
DB 181 TGSNIDCEKLRFRFSLHFMVEVKGLTAKKMWLALLLALRODHGALDCCVVVILSHGCQ 240
QY 241 ASHLQFPFPGAVYGTDCPVSVSEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFVAS 300
DB 241 ASHLQFPFPGAVYGTDCPVSVSEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFVAS 300
QY 301 TSPDESPGSPNEPDATPFQGLRTPDQDLAISLTPSDIPVSTPFGFVSWRDPKSG 360
DB 301 TSPDESPGSPNEPDATPFQGLRTPDQDLAISLTPSDIPVSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIEFQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKLFKFTS 416
DB 361 SWYVETLDDIEFQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKLFKFTS 416

RESULT 2
ICE3_CRILLO STANDARD; PRT; 277 AA.
AC Q60431;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
DE (SCA-1).
GN CASP3 OR CPP32.
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96183185; PubMed=8605870;
RA Wang X., Zelenski N.G., Yang J., Sakai J., Brown M.S.,
RA Goldstein J.L.;
RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by
RT CPP32 during apoptosis.";
RL EMBO J. 15:1012-1020(1996).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
CC element binding proteins (SREBPs) between the basic helix-loop-
CC helix leucine zipper domain and the membrane attachment domain.
CC Cleaves and activates caspase-6, -7 and -9 (By similarity).
CC -!- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- FTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
```

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT GLU-190.
RC TISSUE=t-cell;
RX MEDLINE=95074098; PubMed=7983002;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RT "CPP32, a novel human apoptotic protein with homology to
RT Caenorhabditis elegans cell death protein Ced-3 and mammalian
RT interleukin-1 beta-converting enzyme.";
RL J. Biol. Chem. 269:30761-30764(1994).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=95292347; PubMed=7774019;
RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
RA Beidler D.R., Fokier G.G., Salvesen G.S., Dixit V.M.;
RT "Famsa/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
RT protease that cleaves the death substrate poly(ADP-ribose)
RT polymerase.";
RL Cell 81:801-809(1995).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=95292347; PubMed=7774019;
RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
RA Beidler D.R., Fokier G.G., Salvesen G.S., Dixit V.M.;
RT "Famsa/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
RT protease that cleaves the death substrate poly(ADP-ribose)
RT polymerase.";
RL Cell 81:801-809(1995).
RN [4]
RN SEQUENCE FROM N.A., AND VARIANT GLU-190.
RX MEDLINE=95292347; PubMed=7774019;
RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
RA Beidler D.R., Fokier G.G., Salvesen G.S., Dixit V.M.;
RT "Famsa/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
RT protease that cleaves the death substrate poly(ADP-ribose)
RT polymerase.";
RL Cell 81:801-809(1995).
RN [5]
RN SEQUENCE FROM N.A., AND VARIANT GLU-190.
RX MEDLINE=95292347; PubMed=7774019;
RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
RA Beidler D.R., Fokier G.G., Salvesen G.S., Dixit V.M.;
RT "Famsa/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
RT protease that cleaves the death substrate poly(ADP-ribose)
RT polymerase.";
RL Cell 81:801-809(1995).
RN [6]
RN SEQUENCE FROM N.A., AND VARIANT GLU-190.
RX MEDLINE=95292347; PubMed=7774019;
RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
RA Beidler D.R., Fokier G.G., Salvesen G.S., Dixit V.M.;
RT "Famsa/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
RT protease that cleaves the death substrate poly(ADP-ribose)
RT polymerase.";
RL Cell 81:801-809(1995).
RN [7]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.
RX MEDLINE=9626352; PubMed=8673606;
RA Rotonda J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,
RA Labelle M., Peterson E.P., Rasper D.M., Ruel R., Vaillancourt J.P.,
RA Thornberry N.A., Becker J.W.;
RT "The three-dimensional structure of apocain/CPP32, a key mediator of
RT apoptosis.";
RN [8]
RN Nat. Struct. Biol. 3:619-625(1996).
RX X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.
RP MEDLINE=97197830; PubMed=9045680;
RA Mittl P.R.E., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,
RA Priestle J.P., Tomaselli K.J., Gruetter M.G.;
RT "Structure of recombinant human CPP32 in complex with the
RT tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone.";
RL J. Biol. Chem. 272:6539-6547(1997).
RN [9]
RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=20283632; PubMed=10821855;
RA Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,
RA Kikly K., Winkler J.D., Sung C.M., Debouck C., Richardson S.,
RA Levy M.A., DeWolfe W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,
RA Ryan M.D., Hattiwanger R.C., Liang P.-H., Janson C.A., McDevitt P.J.,
RA Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
RA Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.;
RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7
RT inhibit apoptosis and maintain cell functionality.";
RL J. Biol. Chem. 275:16007-16014(2000).
RN [10]
RN PROCESSING.
RX MEDLINE=96353838; PubMed=8755496;
RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemri E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FADD-like domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
RN [11]
RN CLEAVAGE OF HUNTINGTIN.
RX MEDLINE=96331285; PubMed=8696339;
RA Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,
RA Graham R.K., Bromm M., Kazemi-Esfarjani P., Thornberry N.A.,
RA Vaillancourt J.P., Hayden M.R.;
RT "Cleavage of huntingtin by apocain, a proapoptotic cysteine protease,
RT is modulated by the polyglutamine tract.";
RL Nat. Genet. 13:442-449(1996).
RN [12]
RN FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
CC element binding proteins (SREBPs) between the basic helix-loop-
CC helix leucine zipper domain and the membrane attachment domain.
CC Cleaves and activates caspase-6, -7 and -9. Involved in the
CC cleavage of huntingtin.
CC ENZYME REGULATION: Inhibited by isatin sulfonamides.
CC SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit.
CC SUBCELLULAR LOCATION: Cytoplasmic.
CC TISSUE SPECIFICITY: Highly expressed in lung, spleen, heart, liver
CC and kidney. Moderate levels in brain and skeletal muscle, and low
CC in testis. Also found in many cell lines, highest expression in
CC cells of the immune system.
CC PTM: CLEAVAGE BY GRANTZYM B, APAF-1, CASPASE-6, -8 AND -10
CC GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
CC PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
CC ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
CC OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
CC AND VICE VERSA.
CC SIMILARITY: Belongs to peptidase family C14.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC EMBL; U13737; AAA65015.1; -;
CC EMBL; U13738; AAA60355.1; -;
CC EMBL; U26943; AAA74929.1; -;
CC DR

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DR EMBL: AJ4113269; CAC89866.1; -.
DR EMBL: AY219866; A025654.1; -.
DR EMBL: BC016926; AAH16926.1; -.
DR PIR: A55315; A55315.
DR PDB: 1PAU; 07-JUL-97.
DR PDB: 1CP3; 24-DEC-97.
DR PDB: 1GFW; 23-JUN-00.
DR MEROPS: C14.003; -.
DR Genew; HGNC:1504; CASP3.
DR MIM; 600636; -.
DR GO: GO:0004208; F:caspase-3 activity; TAS.
DR GO: GO:0008624; P:induction of apoptosis by extracellular sig. . ; TAS.
DR GO: GO:0008629; P:induction of apoptosis by intracellular sig. . ; TAS.
DR GO: GO:0009405; P:pathogenesis; TAS.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; IL1RCENZYM.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR KX Hydrolase; Thiol protease; Zymogen; Apoptosis; Polymorphism;
KW 3D-structure.
FT PROPEP 1 9
FT PROPEP 10 28
FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
FT ACT_SITE 121 121 BY SIMILARITY.
FT ACT_SITE 163 163 BY SIMILARITY.
FT VARIANT 190 190 D -> E (in isoform beta).
FT CONFLICT 31 36 ISLDSNS -> MSWDTG (IN REF. 3).
FT STRAND 36 36
FT STRAND 43 51
FT HELIX 57 59
FT TURN 60 60
FT TURN 65 66
FT TURN 67 80
FT TURN 81 82

Query Match
Best Local Similarity 19.2%; Score 418; DB 1; Length 277;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;
QY 150 DLAYILSEPCGHCLIIINNVFCRESGLRTRTGSNIDCEKLRFRFSSLHFVVEVKGDLTA 209
Db 34 DNSYKMDYFEMGLCLIIINNVFKHSTGTSRSGTDVDAANLRETRNLKYEVRNNDLTR 93
QY 210 KMWVALLLELARQDHGALDCCVWILSHGCAQSHLQFPFGAVYGTDCGCVSVKIVNIFNG 269
Db 94 EEIVELMRDVSXEDSHKSRSFVCLLSHGEE-----GIIFGTNG-PVDLKKIINFRFG 145
QY 270 TSCPSLGGKPKLFFQACGGEQKHGFVASTSPDESGPSNPEPDATFPQGLTFDQL 329
Db 146 DCRSLTGKPKLFFIQAACRGTELDGCIETDSCVDDDM----- 182
QY 330 DAISLPLTPSDFVSYSTFPGVSVRYETLDDIFDFAWAHSEDLSQLLRVAN 389
Db 183 -ACHKIPVDALYAYSTAPGYVSRNSKDGWFIQSLCAMLKQYADKLEFHHILTRVNR 241
QY 390 AVSVK-----GIYKMGPCFNFLRKLFF 413
Db 242 KVATEFESFSDATFHANKQIEFIVSMLTKELF 275

RESULT 4
ID ICE3 MOUSE
AC P70677; 008668; Q9QW14;
DT 01-NOV-1997 (Rel. 35, Created)

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DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (CASP-3) (GREBP cleavage activity 1)
DE (SCA-1) (LICE).
DE CASP3 OR CPP32.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358624; PubMed=8761296;
RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RA Fletcher F.A.;
RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
RT a cysteine protease resembling interleukin-1 beta converting enzyme
RT and CED-3.";
RL Oncogene 13:749-755 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224429; PubMed=9070890;
RA Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.;
RT "Specific expression of CPP32 in sensory neurons of mouse embryos and
RT activation of CPP32 in the apoptosis induced by a withdrawal of
RT NGF.";
RL Biochem. Biophys. Res. Commun. 231:770-774 (1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C3H/An.
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenaabeele P., Declercq W., van den Brande I.,
RA van Ioo G., Molemans F., Schotte P., van Criekeinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69 (1997).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fallon J., Heltun E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Rouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RP SEQUENCE OF 58-277 FROM N.A.
RA Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,
RA Fortin J.-P., Sekaly R.-P.;
RT "Multiple pathways of apoptosis converging on the CPP32 protease.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it

```

CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
 CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
 CC element binding proteins (SREBPs) between the basic helix-loop-
 CC helix leucine zipper domain and the membrane attachment domain.
 CC Cleaves and activates caspase-6, -7 and -9 (By similarity).
 CC Cleaves IL-1 beta between an Asp and an Ala, releasing the mature
 CC cytokine which is involved in a variety of inflammatory processes.
 CC -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Highest expression in spleen, lung, liver,
 CC kidney and heart. Lower expression in brain, skeletal muscle and
 CC testis.
 CC -1- PTM: CLEAVAGE BY GRANZYME B. CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family C14.

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 CC or send an email to license@isb-sib.ch).

DR EMBL; U54803; AAC52768.1; -;
 DR EMBL; U54802; AAC52768.1; JOINED.
 DR EMBL; U49929; AAC52764.1; -;
 DR EMBL; D86352; BAA21727.1; -;
 DR EMBL; Y13086; CAA73528.1; -;
 DR EMBL; U19522; AAC53196.1; -;
 DR EMBL; BC038825; AAB38825.2; -;
 DR EMBL; U63720; AAD09504.1; -;
 DR PIR; JC5410; JCS410.
 DR HSSP; P42574; IPAU.
 DR MEROPS; C14.003; -;
 DR MGD; MGI:107739; Casp3.
 DR InterPro; IPR002138; ICE p10.
 DR InterPro; IPR001309; ICE p20.
 DR InterPro; IPR002398; Peptidase C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; IUIBENZIME.
 DR SMART; SM00115; CASc; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 9
 FT CHAIN 10 28 BY SIMILARITY.
 FT CHAIN 129 175 APOAIN P17 SUBUNIT.
 FT CHAIN 176 277 APOAIN P12 SUBUNIT.
 FT ACT_SITE 121 121
 FT ACT_SITE 163 163 BY SIMILARITY.
 FT CONFLICT 17 17 E -> G (IN REF. 2).
 FT CONFLICT 51 51 N -> T (IN REF. 2).
 FT CONFLICT 63 65 SRS -> ARN (IN REF. 6).
 FT CONFLICT 84 84 Q -> E (IN REF. 2).
 FT CONFLICT 95 95 D -> E (IN REF. 2).
 FT CONFLICT 97 97 L -> M (IN REF. 2).
 FT CONFLICT 128 128 Y -> F (IN REF. 2).
 FT CONFLICT 135 135 E -> D (IN REF. 2).
 FT CONFLICT 231 231 E -> Q (IN REF. 6).
 FT CONFLICT 262 262 I -> F (IN REF. 6).
 SQ SEQUENCE 277 AA; 31474 MW; CB91598F74826605 CRC64;

Query Match 19.2%; Score 418; DB 1; Length 277;

Best Local Similarity 32.8%; Pred. No. 3.5e-28;

Matches 90; Conservative 50; Mismatches 92; Indels 42; Gaps 4;

QY 150 DLAYILSMPCGCHLIINNVNFCRBESGLTRTGSNIDCEKLRERFESSLHFMVEVKGDLTA 209
 DB 34 DSSYKMDYDPMGICILINNNKFKHSTGMSRSGTDVDAANLRETFMLGLKIQVRKNKDLTR 93
 QY 210 KKMVLALLBLAQDHGALDCCVVVILSHGCGQASHLQFGAVYGTDCGPVSVEKIVNIFNG 269
 DB 94 EBILELMDSVSKEDHSKRSFVCVILSHGDE-----GVYGTNG-PVELKKLTSFFRG 145
 QY 270 TGCPISGGKPKLFFIQAOCGGEKDHGFVASTSPEDSPGSPNPEDATPFQEGRLTFDQL 329
 DB 146 DYCRSLTGPKLFIQAOCRGTELDGIEDTSGTDEE----- 182
 QY 330 DAISSTPTSDIFVSYSTPFGVSNEDPKSGWYVETLDDIPEQMAHSDQLQSLLRVAN 389
 DB 183 -ACQKIPVEDFLYAYSTAGYISWRNSKDGWFIOQLCSMLKLYAHKLEFHMILTRVNR 241
 QY 390 AVSVK-----GIYKQMPGCFNLRKKLFF 413
 DB 242 KVATEFESFLDSTPHAKKQIPCVSMLTJELVF 275

RESULT 5

ICE3_RAT STANDARD; PRT; 277 AA.
 ID ICE3_RAT P55213; P70543; P97699; O62993;
 AC P55213; P70543; P97699; O62993;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
 DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
 DE (SCA-1) (LICE) (IRP).
 GN CASP3 OR CPP32.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 CX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96358624; PubMed=8761296;
 RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RA Fletcher F.A.;
 RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
 RT a cysteine protease resembling interleukin-1 beta converting enzyme
 RT and CED-3";
 RL Oncogene 13:749-755 (1996).
 RN [2]
 RP SEQUENCE OF 30-241 FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=96042508; PubMed=7588240;
 RA Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I.,
 RA Hirschfield A.N., Tilly J.L.;
 RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and
 RT mammalian cell death: dissociation of IRP-induced oligonucleosomal
 RT endonuclease activity from morphological apoptosis in granulosa cells
 RL of the ovarian follicle";
 RL Endocrinology 136:5042-5053 (1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97184204; PubMed=9030616;
 RA Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K.,
 RA Rostack P.Jr., Poirier G.G., Paul S.M.;
 RT "Cloning and expression of a rat brain interleukin-beta-converting
 RT enzyme (ICE)-related protease (IRP) and its possible role in
 RT apoptosis of cultured cerebellar granule neurons.";
 RL J. Neurosci. 17:1561-1569 (1997).
 RN [4]
 RP SEQUENCE OF 1-264 FROM N.A.
 RA Yakovlev A.G.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. At the onset of apoptosis it

CC CPP32. PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32. PROTEASE ALSO OCCUR AND
CC VICE VERSA.
CC
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC
CC EMBL; U39613; AAC50346.1; -.
CC EMBL; U40281; AAC50352.1; -.
CC EMBL; U37448; AAC50303.1; -.
CC EMBL; U37449; AAC50304.1; -.
CC EMBL; U67319; AAC51152.1; -.
CC EMBL; U67320; AAC51153.1; -.
CC EMBL; U67206; AAF21460.1; -.
CC EMBL; BC015799; AAHL5799.1; -.
CC PDB; 1FIJ; 23-MAY-01.
CC PDB; 1GFJ; 04-JAN-02.
CC PDB; 1IAO; 31-OCT-01.
CC PDB; 1I51; 23-FEB-02.
CC PDB; 1K86; 21-NOV-01.
CC PDB; 1K88; 21-NOV-01.
CC PDB; 1KWC; 16-JAN-02.
CC MEROPS; C14.004; -.
CC Genew; HGNC:1508; CASP7.
CC MW; 601761; -.
CC GO; GO:0005737; C:cytoplasm; TAS.
CC GO; GO:0008234; F:cysteine-type peptidase activity; TAS.
CC GO; GO:0008632; P:apoptotic program; TAS.
CC InterPro; IPR002138; ICE p10.
CC InterPro; IPR001109; ICE p20.
CC InterPro; IPR002398; Peptidase_C14.
CC Pfam; PF00656; Peptidase_C14; 1.
CC PRINTS; PR00376; ILIBCEZYME.
CC SMART; SM00115; CASC; 1.
CC PROSITE; PS01122; CASPASE_CYS; 1.
CC PROSITE; PS01121; CASPASE_HIS; 1.
CC PROSITE; PS0207; CASPASE_P10; 1.
CC PROSITE; PS0208; CASPASE_P20; 1.
CC Hydrolase; Thiol protease; Zymogen; Apoptosis; Alternative splicing;
CC 3D-structure.
CC FT PROPEP 1 23
CC FT CHAIN 24 198
CC FT PROPEP 199 206
CC FT CHAIN 207 303
CC FT ACT_SITE 144 144
CC FT ACT_SITE 186 186
CC FT VARSPPLIC 1 1
CC
CC FT VARSPLIC 149 303
CC
CC FT MUTAGEN 186 186
CC FT CONFLICT 4 4
CC FT CONFLICT 194 194
CC FT SEQUENCE 303 AA; 34276 MW; CD373EB54A232CA4 CRC64;
CC
CC Query Match 16.6%; Score 361.5; DB 1; Length 303;
CC Best Local Similarity 33.3%; Pred. No. 2.6e-23;
CC Matches 92; Conservative 41; Mismatches 94; Indels 49; Gaps 8;
CC
CC 153 YILSMEPOGHCLIIINNVPFCRESGLNTRTGSNIDCEKLRRFSSLHFMVYKGLDTAKKM 212

DB 60 YNNFEKLGKCIINNKNFVKVTGNGVNGHDKDAEALFKCFSRLGFDVIVYNDSCAKM 119
QY 213 VLALLELARQDHGALDCVWVILSHGCOASHLPFGAVYGTGCGFVSVEKVNIFNGTSC 272
DB 120 QDLIKASEEDHTWAACFACILLSHGEE-----NVIYKDGVTPIKDLTAHPRGDR 171
QY 273 PSLGGKPKLFFIQACGGQKDHGFEVASTSPEDSPGSPNPFDPATPFQEGRLTFDQDAI 332
DB 172 KTLLEKPKLFFIQACRGTELDGIGQADS-----GPINDTDANPRYK----- 212
QY 333 SSLTPSPDIFVSYSTFPFCFVSWRDPKSCSWVETLDDIFEQWASEDIQ--SLLLRVANA 390
DB 213 --IPVEADFLFAYSTVPFGYSWRSPGRGSWVQALCSILEE--HGKDLIMQILTRVNR 268
QY 391 VS-----VKGIYKQMPGCFNFKKLPFF 413
DB 269 VARHPESQSDDPHFHEK---KQIPCVVSMLTKELYF 301

RESULT 8
ICE7 MOUSE
ID ICE7 MOUSE STANDARD; PRT; 303 AA.
AC P97864; O08669;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine protease) (Apoptotic
DE protease Mch-3).
GN CASP7 OR MCH3 OR LICE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] _
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Fletcher F.A.;
RT "Identification and mapping of Casp7, a cysteine protease resembling
RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
RL Genomics 40:86-93 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97236307; PubMed=9125129;
RA Mukasa T., Khoroku Y., Tsukahara T., Momoi M.Y., Kimura I.,
RA Momoi T.;
RT "Wortmannin enhances CPP32-like activity during neuronal
RT differentiation of P19 embryonal carcinoma cells induced by retinoic
RT acid.";
RL Biochem. Biophys. Res. Commun. 232:192-197 (1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
RA van Loo G., Molemans F., Schotte P., van Criekeinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69 (1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max J.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,


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FT CHAIN 187 282 APOAIN P12 SUBUNIT.
FT ACT SITE 131 131 BY SIMILARITY.
FT ACT SITE 174 174 BY SIMILARITY.
SQ SEQUENCE 282 AA; 32124 MW; CB390E6980CAB77F CRC64;

Query Match 16.0%; Score 349; DB 1; Length 282;
Best Local Similarity 31.4%; Pred. No. 2,7e-22;
Matches 81; Conservative 45; Mismatches 94; Indels 38; Gaps 6;

QY 161 GHLIINNVNFCRESGLRTGTSGNIDCEKLRFRFSSLHFWVEYKGLDTAKKMWLALLELA 220
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 56 GMCLIIINNVNFCRESGLRTGTSGNIDCEKLRFRFSSLHFWVEYKGLDTAKKMWLALLELA 114
QY 221 RQHGALDCCVVILSHGCOASHLPFGAVYGTGCVSVVEKIWNIFNGTSCPSLOGKPK 280
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 115 EEDHKKRSFVCAILSHG-----EEDGSCGVVD-VPIHIKNTDLFRGRCKTLVGKPK 167
QY 281 LFTIQACGGKQKHGFEVASTS-PEDESFGSNPEPDATPQEGRLTFDQLDAISLPTPS 339
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 168 IFFIQACRGTELDSTGIEDTSCSEPRE-----IQRIPEVA 202
QY 340 DIFVSYSTRPGFVSRDPKSGSVVETLDDIFQWHAHSEDLQSLLLRVANAVSVK---G 395
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 203 DFLYATSTVPGYCWDRKMDGMSFQISLCKMIKLYGSHLELIQLITCVNMVVALDFTFH 262
QY 396 IYKQMPGCFNFRKKLFF 413
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 263 AKQIPCVSMVLTGSFYF 280

RESULT 10
ICE DROME STANDARD; PRT; 339 AA.
AC O01382: Q9VAH1;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase precursor (EC 3.4.22.-) (drice).
GN ICE OR C67788.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_Taxid=7227;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RC MEDLINE=97327558; PubMed=9184225;
RX Fraser A.G., Evan G.I.;
RA "Identification of a Drosophila melanogaster ICE/CED-3-related
RT protease, drICE."
RL EMBO J. 16:2805-2813 (1997).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=Berkley;
RC MEDLINE=20196006; PubMed=10731132;
RX Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G.G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Butler H., Cadieu E., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

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RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houch J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinart K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.H.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
RN [3]
RN SEQUENCE FROM N.A.
RP STRAIN=Berkley; TISSUE=Head;
RC MEDLINE=22426086; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarini H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celnik S.E.;
RT "A Drosophila full-length cDNA resource."
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Acts downstream of rpr.
CC Cleaves baculovirus p35 and lamin Dmo in vitro.
CC -!- SUBUNIT: Heterodimer of a 21 kDa (p21) and a 12 kDa (p12) subunit.
CC -!- DEVELOPMENTAL STAGE: Expressed at all stages where apoptosis
CC occurs.
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y12261; CAA72937.1; -
CC EMBL; AE003771; AAF56939.1; -
CC EMBL; AY058451; AAL13680.1; -
CC HSP; P42574; 1PAU.
CC MEROPS; C14.015; -
CC FlyBase; FBgn0019972; Ice.
CC GO; GO:0004207; F:effector caspase activity; NAS.
CC GO; GO:0006915; P:apoptosis; NAS.
CC InterPro; IPR001309; ICE_p10.
CC InterPro; IPR002398; Peptidase_C14.
CC Pfam; PF00656; Peptidase_C14; 1.
CC PRINTS; PR00376; IL1BCENZYME.
CC SMART; SM00115; CASc; 1.
CC PROSITE; PS01122; CASPASE_CYS; 1.
CC PROSITE; PS01121; CASPASE_HIS; 1.
CC PROSITE; PS02027; CASPASE_P10; 1.
CC PROSITE; PS02028; CASPASE_P20; 1.
CC Hydrolase; Thiol protease; Zymogen; Apoptosis.
KW PROPEP 1 28 BY SIMILARITY.
FT CHAIN 29 217 CASPASE SUBUNIT P21 (BY SIMILARITY).
FT PROPEP 218 230 BY SIMILARITY.
FT CHAIN 231 339 CASPASE SUBUNIT P12 (BY SIMILARITY).
FT ACT_SITE 169 169 BY SIMILARITY.
FT ACT_SITE 211 211 BY SIMILARITY.
FT CONFLICT 151 151 A -> S (IN REF. 1).
FT CONFLICT 265 265 S -> T (IN REF. 1).

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SQ SEQUENCE 339 AA; 37363 MW; E105ED29518507EC CRC64;
Query Match 14.9%; Score 324; DB 1; Length 339;
Best Local Similarity 29.0%; Pred. No. 4.7e-20;
Matches 90; Conservative 37; Mismatches 123; Indels 60; Gaps 6;

QY 115 IRKPEVLRETPTVDIGSGGSDVCAI-----ESLRNA-- 149
DQ 17 VGNPEQNDHTDALGVSAGSGAGSLVAGSHYPSGGAIGOLANGYSPSPSYRKNVAK 76
QY 150 -----DLAYILSMPCGCHLIINNVCRESGLRTRTGSNIDCEKLRERFSLHFMVEV 203
DQ 77 MYTDRHAEYNNRKNRGWALFNHEHF-EVTLKSRAGTNDNCNLTFLVKQLDFEVTV 135
QY 204 KGLTAKMVLALLEAROHGALDCVVLVILSHGCOASHLQPPGAVGTGDCPVSVKRI 263
DQ 136 YKDCRYKDLRTIEVAASQNSHSDCILVAILSHGEM-----GVYAKD-TQYKLDNI 187
QY 264 VNIENGTSCPSLGGKPKLFFIOACGGEQKHGFVASTSPEDSPGSPNPEPDATPQBL 323
DQ 188 WSEFTANHCPSLAGPKLFFIOACGQDRLDGGVTWQRTOTETDGDSS----- 234
QY 324 RTFDQDAISSFTSPDIFVSYSTFPFGVSWDRPKSGMYVETLDDIFQWHAHSDLOS 383
DQ 235 -----MSYKIPVHDFLIAYSTVPGFYSWNTTSGWFMQSLCAELAAANGKRLDILT 287
QY 384 LLRVANAVSV 393
DQ 288 LTFVCQVAV 297

RESULT 11
ICE6 MOUSE STANDARD; PRT; 276 AA.
ID ICE6 MOUSE STANDARD; PRT; 276 AA.
AC 008738;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
GN CASP6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
RA van Leeuwen G., Molenans F., Schotte P., van Crielinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves poly(ADP-ribose)
CC polymerase in vitro, as well as lamins. Overexpression promotes
CC programmed cell death (By similarity).
CC -!- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 11 kDa (p11) subunit
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Highly expressed in lung, liver, kidney,
CC testis, and heart. Lower levels in spleen, skeletal muscle and
CC brain.
CC -!- PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
CC SUBUNITS (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; Y13087; CAA73529.1; -.
DR HSP; P42574; LPAU.
DR MEROPS; C14.005; -.
MGD; MGI:1312921; Casp6.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase C14.
PFam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILIBCEZYME.
SMART; SM00115; CASP; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02077; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 5
FT CHAIN 6 162
FT CASPASE-6 SUBUNIT P18 (BY SIMILARITY).
FT PROPEP 163 176
FT CHAIN 177 276
FT CASPASE-6 SUBUNIT P11 (BY SIMILARITY).
FT ACT_SITE 104 104
FT ACT_SITE 146 146
FT ACT_SITE 146 146
FT ACT_SITE 146 146
SQ SEQUENCE 276 AA; 31595 MW; 5665DE932112686C CRC64;

Query Match 14.8%; Score 322; DB 1; Length 276;
Best Local Similarity 33.1%; Pred. No. 5.2e-20;
Matches 88; Conservative 39; Mismatches 103; Indels 36; Gaps 9;

QY 161 GHCLINNVNFCRSGRLTRTGSNIDCEKLRERFSLHFMVEVKGDLTAKMVLALLEA 220
DQ 28 GVALIFNHERFVHLTLPERGTNADRLNLTFRFSDGLGFEVKCFNDLRAEELLKHEVS 87
QY 221 RQDHGALDCVVLVILSHGCOASHLQPPGAVGTGDCPVSVKIVNIENGTSCPSLGGKPK 280
DQ 88 TSSHIDADCFCVFLSHG-EGNH-----VYAYD-AKIEITLTGLFGDKQCSLVGKPK 139
QY 281 LFFIQACGGEQKHGFVASTSPEDSPGSPNPEPDATPQBLRTFDQDAIS--SLPTP 338
DQ 140 IFIICAKGSGQ--HDVPVPLDMVDHQ-----TDKLDNVTQVDAASVVTLPAG 185
QY 339 SDIFVSYSTFPFGVSWDRPKSGMYVETLDDIFQWHAHSDLOSLLLVANAVSVKGI-- 396
DQ 186 ADFLMCVSAEGYSHRETVNGSVYIQLCEMLARYSGSLEFTELLTLVNRKVSRRVDF 245
QY 397 -----YKOMPQCF-NFLRKLFF 413
DQ 246 CKDPDAIGKKQVP-CFASMLTKLHF 270

RESULT 12
ICE1 DROME STANDARD; PRT; 323 AA.
ID ICE1 DROME STANDARD; PRT; 323 AA.
AC 002002; OSW1N0;
DT 15-JUN-1998 (Rel. 35, Created)
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-1 precursor (EC 3.4.22.-).
GN DCP-1 OR CG5370.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 216-248.
RC TISSUE=Embryo;
RX MEDLINE=97153052; PubMed=899799;
RA Song Z., McCall K., Steiller H.;
RT "DCP-1, a Drosophila cell death protease essential for development.";
RL Science 275:536-540(1997).
RN [2]
RP ERRATUM.
```



```
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
PROCESSING.
TISSUE=Lymphocytes;
MEDLINE=97059171; PubMed=890201;
RA Strinivasula S.M., Fernandes-Alnemri T., Zangrilli J., Robertson N.,
RA Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,
RA Alnemri E.S.;
RT "The Ced-3/interleukin 1beta converting enzyme-like homolog Mch6 and
RT the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic
RT mediator CPP32.";
RL J. Biol. Chem. 271:27099-27106(1996).
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves poly(ADP-ribose)
CC polymerase in vitro, as well as lamins. Overexpression promotes
CC programmed cell death.
CC -!- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 11 kDa (p11) subunit.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Name=Alpha;
CC IsoId=p55212-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=p5212-2; Sequence=VSP_000805;
CC -!- PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
CC SUBUNITS.
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
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```

Search completed: August 3, 2004, 09:01:51
Job time : 14 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 08:58:51 ; Search time 39 Seconds
(without alignments)
3365.527 Million cell updates/sec

Title: US-09-961-201a-1
Perfect score: 2180
Sequence: 1 MDEADRLRLRCRLRLVEEL.....YKMPGCFNLRKLLFFKTS 416

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 789523

Minimum DB seq length: 0
Maximum DB seq length: 416

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 25: *
1: sp_archea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacterioph: *
17: sp_archeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1336	61.3	393	11 Q9R0S9	Q9R0S9 mus musculus
2	1093	50.1	383	11 Q99M88	Q99M88 rattus norv
3	1048.5	48.1	399	13 Q9IB63	Q9IB63 xenopus lae
4	1000.5	45.9	403	13 Q90WU0	Q90WU0 gallus gall
5	613	28.1	229	11 Q7TQC1	Q7TQC1 rattus norv
6	485	22.2	177	11 Q92UG4	Q92UG4 rattus norv
7	437	20.0	313	11 Q8CHV5	Q8CHV5 mus musculus
8	435	20.0	316	5 Q8I7B0	Q8I7B0 geodia cydo
9	421	19.3	328	5 Q8ITP3	Q8ITP3 brachiosto
10	420	19.3	277	6 Q95ND5	Q95ND5 sus scrofa
11	419	19.2	277	6 Q8MJU1	Q8MJU1 felis silve
12	418	19.2	280	13 Q8JGM9	Q8JGM9 fugu rubrip
13	413	18.9	280	13 Q8JG42	Q8JG42 fugu rubrip
14	402.5	18.5	318	13 Q9IB65	Q9IB65 xenopus lae
15	401	18.4	277	6 Q8MKI5	Q8MKI5 canis fami
16	401	18.4	277	6 Q8MUC3	Q8MUC3 oryctolagus

ALIGNMENTS

RESULT 1

Q9R0S9 ID Q9R0S9 PRELIMINARY; PRT; 393 AA.
AC Q9R0S9;
DT 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Caspase9S.
GN CASP9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20001956; PubMed=10529400;
RA Fujita E., Jinbo A., Matuzaki H., Konishi H., Kikkawa U., Momoi T.;
RT "Akt phosphorylation site found in human caspase-9 is absent in mouse
caspase-9".
RL Biochem. Biophys. Res. Commun. 264:550-555(1999).
DR EMBL; AB019601; BAA86896.1; -;
DR HSSP; P42574; IPAU.
DR MEROPS; C14.010; -;
DR MGD; MGI:1277950; Casp9.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILLBCENZME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.

Q93417 gallus gall
Q98ui8 brachydanio
Q8jis9 oryzias lat
Q8jis8 oryzias lat
Q80im6 xenopus lae
Q88550 rattus norv
O77623 ovis aries
Q86f10 anopheles s
Q8itp2 brachiosto
Q93415 gallus gall
Q99m47 mus musculu
Q9d889 mus musculu
Q9ib66 xenopus lae
Q8bnt4 mus musculu
Q35397 rattus norv
Q9gv88 hydra atten
Q9wiu6 rattus norv
Q8eu33 homo sapien
Q8i9v7 bombyx mori
Q8i955 spodoptera
Q9i8s9 oncorhynchu
Q9vet9 drosophila
Q9nhf9 drosophila
Q8k4i9 meriones un
Q9lw32 rattus norv
Q9tzp5 caenorhabdi
Q9i917 brachydanio
Q9gv89 hydra atten
Q9tzp6 caenorhabdi

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DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02008; CASPASE_P20; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02008; CASPASE_P20; 1.
SQ SEQUENCE 393 AA; 42975 MW; CA889475B50DD632 CRC64;

Query Match
Best Local Similarity 61.3%; Score 1336; DB 11; Length 393;
Matches 267; Conservative 26; Mismatches 57; Indels 38; Gaps 2;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFPRPHMIEDIQAGSGSRDDQARQLII 60
DB 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFPRPHMIEDIQAGSGSRDDQARQLII 60
QY 61 DLETRGSAALPLFISCLDGTQDMLASFLRTNRQAGKL----- 98
DB 61 DLETRGSAALPLFISCLDGTQDMLASFLRTNRQAGKL----- 98
QY 99 -----SKPTLENLTTPVLRPE-----IRKPEVLRPETPRPVDIGSGGFGDVGAL 120
DB 121 AKEQKRVKLEPSQAVGNLTTPVLRPEELWPARKPEVLRPETPRPVDIGSGGAGHDVCP 180
QY 143 ESLRGNADLAYILSMPCGHCLIIINNVCRESGLRTGNSIDCEKLRRLRPSLHFVWE 202
DB 181 GKIRHADWAYTLSDPCGHCLIIINNVCRESGLRTGNSIDCEKLRRLRPSLHFVWE 240
QY 203 VKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCCOASHLOFFGAVYGTDCGCPVSVEK 262
DB 241 VKNDLTAKKMWLTALMEMAHRNHRALDCCFVVVILSHGCCOASHLOFFGAVYGTDCGCSVIEK 300
QY 263 IVNIFNGTSCPSLGGKPKLFFTIQACGGQKHGFVASTSPEDSGNBPDPATPFQEG 322
DB 301 IVNIFNGTSCPSLGGKPKLFFTIQACGGQKHGFVASTSPEDSGNBPDPATPFQEG 360
QY 323 LRTFDOLDALISLTPSDFVSYSTFPG 350
DB 361 PRPLDQDAVSSLPSTPFDILVSYSTFPG 389

RESULT 2
Q99M88 PRELIMINARY; PRT; 383 AA.
AC Q99M88;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Caspase-9 CTD isoform.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21192275; PubMed=11278518;
RA Angelastro J.M., Moon N.Y., Liu D.X., Yang A.-S., Greene L.A.,
RA Franke T.F.;
RT "Characterization of a Novel Caspase-9 Isoform in Rat That Inhibits
RT Apoptosis.";
RL J. Biol. Chem. 276:12190-12200(2001).
DR EMBL; AY008275; AAG21690.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.010; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCENZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.

RESULT 3
Q9IB63 PRELIMINARY; PRT; 399 AA.
AC Q9IB63;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Caspase-9.
GN XCASPASE-9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yaoita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family.";
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038172; BAA94750.1; -.
DR HSSP; Q15806; 1QDU.
DR MEROPS; C14.010; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0007185; P:signal transduction; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR000488; Death.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCENZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; PR00376; ILIBCENZYME.
```

DR	SMART; SM001114; CARD; 1.
DR	SMART; SM001115; CASC; 1.
DR	PROSITE; PS50269; CARD; 1.
DR	PROSITE; PS01122; CASPASE_CYS; 1.
DR	PROSITE; PS01121; CASPASE_HIS; 1.
DR	PROSITE; PS50207; CASPASE_P10; 1.
DR	PROSITE; PS50208; CASPASE_P20; 1.
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.
SQ	SEQUENCE 399 AA; 44772 MW; EE2A269719064F9F CRC64;

Query Match	48.1%; Score 1048.5; DB 13; Length 399;
Best Local Similarity	51.8%; Pred. No. 1.Se-85;
Matches 216; Conservative 67; Mismatches 113; Indels 21; Gaps	

QY	1	MDEADRLRRCLRULVEELQVDLWVLLSRFLFRPHMIEDIQAGSGRRDQAQLII	60
Dd	1	MEQEILDIRNRVLVQSLOVKELDWLLVERGVFSNDMIEIQR--EGTRRDQARKLV	58
QY	61	DLETRGSAQLPLFI SCHE DTGDMDLASFRTNROAGKLSKETLENLT PVVLRPEIRKEPV	120
Dd	59	ELETGRSQAFPLFLCLIKETAQHDLADFQSD-SGTRVLQPIPTTSP-VLK P--- LPKA	113
QY	121	LRPETPRVDIGSGFGDVGALESRG--NADLAVILSWEPCHGLIINN VNF CRESGLR	178
Dd	114	EPASYP-----AREIRSKGTLDKKDYPMSSDIGFC LIINN NHFECTGLS	161
QY	179	TRTGSNIDCEKLRRFFSLHFWVEVKGDLTAQMVLALLEARQDHGALDC CVV VILSHG	238
Dd	162	TETGSDIDRDKLANMRSFHEVTVKDNLTGMHDHLQALADQDHS LQDCCLV VILSHG	221
QY	239	QOASHLPQPGAVYGTDGCPVSVEKI VNTFN GTS CP SLGGKPKLFIOACGGCKDHGEV	298
Dd	222	CETRHIQPPGYVGTDGRI PVERIVSV FNGSKCPSLGKPKIFI IOACGGCK OQKGEV	281
QY	299	ASTSPEDSPGSNPBPDATPFQEG LRTEDQ DAISSLTPPSIFVSYS TFPF GVSWRDPK	358
Dd	282	TSETPLPLEPTSLQSDATVPFSGEGRDEVDAVNSIPTPS DI LYSYSTFP GV SWRDKH	341
QY	359	SGSWVETLDDIFEQWAHSEDI QSILLR VANAVSVKGIYQMPGPCNF RKKL PFKT	415
Dd	342	TCSWYEVILDSVLAEEAAADDLS ILVM ADVSSKGT YKQIP GFENF LRKE RYFT	398

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RESULT 4
Q90WUO
ID Q90WUO PRELIMINARY; PRT; 403 AA.
AC Q90WUO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 9 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Barton S., Brigham J.T., Johnson A.L.;
RT "Caspase-8 and -9 expression in the hen ovary.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY057940; AAL23701.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006915; F:apoptosis; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.

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DR	InterPro; IPR001993; Mitoch_carrier.
DR	InterPro; IPR002398; Peptidase_C14.
DR	Pfam; PF00619; CARD; 1.
DR	Pfam; PF00656; Peptidase_C14; 1.
DR	PRINTS; PR00376; ILIBCEZYME.
DR	SMART; SW00115; CASC; 1.
DR	PROSITE; PS01122; CASPASE_CYS; 1.
DR	PROSITE; PS01121; CASPASE_HIS; 1.
DR	PROSITE; PSS0207; CASPASE_P10; 1.
DR	PROSITE; PSS0208; CASPASE_P20; 1.
DR	PROSITE; PS00215; MITOCH_CARRIER; 1.
FT	NON TER 1
SQ	SEQUENCE 403 AA; 44913 MW; 0F1E40C3E6594FC4 CRC64;

Query Match 45.9%; Score 1000.5; DB 13; Length 403;
 Best local Similarity 55.3%; Pred.No. 3.e-81;
 Matches 208; Conservative 45; Mismatches 100; Indels 23; Gaps 7;

Qy	52	RDOARQLIIDLTRGSOALPLFIACLEDTGDMLASFLRTNRQAGKLSKPTLEMLTPVVL	111
Dd	34	KEQARQLVIDLTRGKAQAFIFLSILRDTGHGDLADML--DEGGCPSPMPDVD-LRPVOL	90
Qy	112	R-PEIRKPE-----VLRPTTR---PVDIGSGGFGDVGALSLRGNADLAYILSM	157
Dd	91	ELPGDRDKSVSTAERLISIPQPESERFRMPAPAQG-----SAVDKSR-PTDWCTSC EQ	144
Qy	158	EPCGHCLIIINNVNFCRSGLRLTRGSNDICPKLRRTSSLFHFMVEVKGLTAKKNVLALL	217
Dd	145	TPCGHCILFINNVSFSRSDLSUSTRAGSDIDCKEKLPRESLCFHVRTLENLXAQEIDVELR	204
Qy	218	ELARDQHGDALDCVVVILLSHGCQASHIQFGAVYGTGCPVSVBKIVNFNGTSCPSLGG	277
Dd	205	KLARLDHSALDCLLVILLSHCQTSHIQFGGIYGTGKIPIERIINVYNFGSQCPSLRG	264
Qy	278	KPKLFFFOACGEQKHGFVASTSPEDSPGNSPEDATPFQGLRFFDOLDATSI SPT	337
Dd	265	KPKLFFIOACGEQKHGFVDCSPQDETCSRISDAIPQAPSGNEDEFDVASLPT	324
Qy	338	PSDI FVSYSTPPGVSWRDPKSGWVETLDDIPEWAHSEDLQLLLLRVANAVSKGIY	397
Dd	325	PGBIILVSYSTPPGVSWRDKVSGWVETLDSVLEHYARSEDLTLKLVRSDIVSSKGRIY	384
Qy	398	KOMPCCFNFLRKLIFF	413
Dd	385	KOIPGCCFNFLRKLIFF	400

```

RESULT 5
Q7TQC1
ID Q7TQC1 PRELIMINARY; PRT; 229 AA.
AC Q7TQC1;
DT 01-OCT-2003 (trEMBLrel. 25, Created)
DT 01-OCT-2003 (trEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (trEMBLrel. 25, Last annotation update)
DE 25 kDa caspase-9 dominant negative protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA Cao G., Wu S., Sheng L., Graham S.H., Zhou Z., Chen J.;
RT "Molecular cloning and characterization of three caspase-9 dominant
RT negative forms in rats.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AV124461; AAC92272.1; -.
SQ SEQUENCE 229 AA; 25194 MW; 87C293AF139F3B23 CRC64;

Query Match 28.1%; Score 613; DB 11; Length 229;
Best Local Similarity 59.7%; Pred. No. 9.1e-47;
Matches 133; Conservative 14; Mismatches 37; Indels 38; Gaps

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QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQAROLII 60
Db 1 MEEADQLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQAROLVI 60
QY 61 DLETRGQALPLFISCLDTGQDLASFLRTNRQAGL----- 98
Db 61 DLETRGQALPLFISCLDTGQDLASFLRTNRQAGL----- 98
QY 99 -----SKPTLENLTPVVLRLPE-----IRKPEVLRLPETERPVDIGSGFGDVGL 120
Db 121 SKEQKVVDLPSPALGNLTPVVLGPEELWFLRLPEVLTPETPRVDIGSGRAHDVCTP 180
QY 143 ESLRGVADLAYILSWPEPOGHILINNPNFCRSLGRLTRTGS 183
Db 181 GKIERHADWAYTLDSDCPGHCPIINNPNFCPSGLSTRIGS 221

RESULT 6
Q920G4
ID Q920G4 PRELIMINARY; PRT; 177 AA.
AC Q920G4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Caspase-9 short form.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA Cao G., Chen D., Ma L., Graham S.H., Chen J.;
RT "Cloning and Characterization of Rat Caspase-9: Implication for a Role
RT in Neuronal Cell Death During Brain Development and Transient Cerebral
RT Ischemia."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF293333; AAK97086.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR001315; CARD.
DR Pfam; PF00619; CARD; 1.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS50209; CARD; 1.
SQ SEQUENCE 177 AA; 19700 MW; E9DCDA77156AD748 CRC64;

Query Match 22.2%; Score 485; DB 11; Length 177;
Best Local Similarity 60.5%; Pred. No. 2e-35;
Matches 107; Conservative 10; Mismatches 22; Indels 38; Gaps 2;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQAROLII 60
Db 1 MEEADQLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQAROLVI 60
QY 61 DLETRGQALPLFISCLDTGQDLASFLRTNRQAGL----- 98
Db 61 DLETRGQALPLFISCLDTGQDLASFLRTNRQAGL----- 98
QY 99 -----SKPTLENLTPVVLRLPE-----IRKPEVLRLPETERPVDIGSGFGDV 139
Db 121 SKEQKVVDLPSPALGNLTPVVLGPEELWFLRLPEVLTPETPRVDIGSGRAHDV 177

RESULT 7
Q8CHV5
ID Q8CHV5 PRELIMINARY; PRT; 313 AA.
AC Q8CHV5;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Caspase 3, apoptosis related cysteine protease (Fragment).
GN CASP3.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RA Strausberg R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC038825; AAH38825.1; -.
DR MGD; MGI:107739; Casp3.
DR GO; GO:0003693; F:caspase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Protease.
FT NON TER
SQ SEQUENCE 313 AA; 35174 MW; 96E98A1F04E769FC CRC64;

Query Match 20.0%; Score 437; DB 11; Length 313;
Best Local Similarity 31.5%; Pred. No. 9.1e-31;
Matches 106; Conservative 52; Mismatches 123; Indels 56; Gaps 5;

QY 87 SFLTNQAGKLSKPTLENTTPVVLRLPEIRKPEVLRPETPRPVDIGSGFGDVGALESLR 146
Db 21 SVLRGAWNGTLRKVTMENNKTSVDSKSIINNFVKTHGSKSVDSGI----- 67
QY 147 GNADLAYILSWPEPCGHCLINNPNVNFRESGLRTRTGSNIDCEKULRRFPSSLHFVVEVKGD 206
Db 68 -YLDSSYKMDYPENGICIIINNNKFNHKSSTGSRGTDVAANLRFTFMGLKYQVRNKND 126
QY 207 LTAKMVLALLELARQDHGALDCCVVVLSHGQASHLPFGVAVYGTGDCPVSVEKIVNI 266
Db 127 LTREDILLELMDSVSKEDHSKRSFVCLSHGDE-----GVITYNG-PVELKULTSF 178
QY 267 FNGTSPSLGCKPLFFIQACGEGKHGFEVASTSPEDSPGSPNPFDPATPFQEGLTFF 326
Db 179 FRGDYCRSLTGKPKLFIQACRGTELDGCTETDSTGTDEN----- 218
QY 327 DQLDAISSLTPSPDIFVSYSTPFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLR 386
Db 219 ----ACQKIPVEADFLYAYSTAGFYYSWRNSKDGSMFIQSLCSMLKLYAHKLFMHILTR 274
QY 387 VANAVSVK-----GIYKMPGCGFNFLRKKLFF 413
Db 275 VNRKVATEFESFLDSTFEHAKQIPICIVSMLTKELYP 311

RESULT 8
Q8I7B0
ID Q8I7B0 PRELIMINARY; PRT; 316 AA.
AC Q8I7B0;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Caspase 3.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Astrophorida; Geodiidae; Geodia.
OX NCBI_TaxID=6047;
RN 1
RP SEQUENCE FROM N.A.
RA Wiens M., Saenger H., Krasko A., Perovic S., Mueller W.E.G.;
RT "Caspase-mediated apoptosis in sponges: cloning and function.";

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Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL: A417903; CAD10676.1; -
DR GO: GO:0030693; F:caspase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; Peptidase C14.
DR Pfam: PF00656; Peptidase C14; 1.
DR PRINTS: PR00376; IL1BCENZYM.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS02027; CASPASE_P10; 1.
DR PROSITE: PS02028; CASPASE_P20; 1.
DR SEQUENCE 316 AA; 35319 MW; 33A46BCCE6C3F9B7 CRC64;
SQ

Query Match 20.0%; Score 435; DB 5; Length 316;
Best Local Similarity 35.1%; Pred. No. 1.4e-30;
Matches 113; Conservative 44; Mismatches 121; Indels 44; Gaps 9

QY 111 LRPEIRKEVLRPETPRPVDIGSGGFDVGALSLRGNADLAYILSMPEPCGHCLINNVN 170
DB 10 VRPLIAPTATSHPPIPPPPEGT----DAGRKD-----AYKSSRRPRGMALLINNRN 57
QY 171 FCRESGLRTRTGSNIDCEKLRFRFSLHPMVEVKGLDTAKQWVLLLELARODHGALDCC 230
DB 58 F--TCGMKEFVGTDXAENLYGLFWLGMATIRKDNLTGKAMTRFEFDLAREHDSAYDCV 115
QY 231 VVVIILSHGCOASHLOFPFGAVYGTDCPVSVEKIVNIFNGTSCPSLGKGKPLFFIOACGGE 290
DB 116 VVAILLTHG-----ISGRLYSTGDGLIFVEDLTKYFDGWNRPRLIGKPKVFWVQACRGG 168
QY 291 QKHGHEVASTSPEDSPGSPNPEPDATPFQEGRLTFDQ-----LDA-----ISSLP 336
DB 169 KFDYGVGESESTDGESESVN---KETANEMME--KQFDKVKVEKALDADETDGGGYSREALP 223
QY 337 TPSDIFVSYSTPPGFGVSWRDPKSGSVYVETLDDIFEQWASEDLQSLLRVANAVSV--- 393
DB 224 TEADFVLVATVDCYGVSWRNSSEYSGVFWFIKAFVDTMRDLASKEHFMDILTVEVRKVVYDFQ 283
QY 394 -KGIVKQMPGCFNLRKRLFFK 414
DB 284 SRGNKGIAPAVTMTLTKLYER 305

RESULT 9
Q8ITP3 PRELIMINARY; PRT; 328 AA.
ID Q8ITP3
AC Q8ITP3; 2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE AmphicASP-3/7.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7739;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22217375; PubMed=12232796;
RA Bayascas J.R., Yuste V.J., Benito E., Garcia-Fernandez J.,
RA Comella J.X.;
RT "Isolation of AmphicASP-3/7, an ancestral caspase from amphioxus
RT (Branchiostoma floridae). Evolutionary considerations for vertebrate
RT caspases";
RL Cell Death Differ. 9:1078-1089(2002).
DR EMBL: AF412335; AAN45649.1; -
DR GO: GO:0030693; F:caspase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; Peptidase C14.
DR Pfam: PF00656; Peptidase C14; 1.

[illegible]

Query Match 19.3%; Score 420; DB 6; Length 277;
Best Local Similarity 32.1%; Pred. No. 2.6e-29;
Matches 88; Conservative 56; Mismatches 88; Indels 42; Gaps 4;
CV 150 DLAYILSMPCGCLLIINNTNFCESGLRTRTGSNIDCEKLRFRFSSLIHFMEVVKDLTA 209

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Db 34 DVSYKMDYFENGGLCIINNNKFDKNTGWACSGTGDVDAANLRETFTNLKYEVRNKDLTR 93
Qy 210 KMWLALLELARQDHGALDCCVVILSHGCOASHLQFPQAVYGTDCGCPVSVEKIVNIFNG 269
Db 94 EILLELHSHSVSKEDHSHKSSFCVLLSHGEE-----GKIFGTNG-PVDLKKLTSPFRG 145
Qy 270 TSCPSLGGKPKLFFIOACGGEKQDHGFVASTSPEDSPGSPNPEPDATPFQGLRTFDQL 329
Db 146 DCCRTLTGKPKLFFIOACRGTELDGCIETDSTGDDM----- 182
Qy 330 DAISLPTSPDIFVSYSTFPFVSWRDPKSGSVVETLDDIFEQWASHEDLSLLLRVAN 389
Db 183 -ACQKIPVEADFLYAYSTAGYYSWRNSKDGSWFIQSLCAALKQYVHKLHMLTRVNR 241
Qy 390 AVSVK-----GIYKMPGCFNFKLFF 413
Db 242 KVAVFESFSTDTSTFHAQKQIPCVISMLTKELF 275

RESULT 11
Q8MJUL PRELIMINARY; PRT; 277 AA.
AC Q8MJUL
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase3.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamazaki J., Sano J., Kano R., Hasegawa A.;
RT "Felis catus mRNA for caspases, complete cds.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB030246; BAC10589.1;
DR GO; GO:0030693; P:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR002138; ICE_p10.
DR PRINTS; PR00376; IL1BCENZYME.
DR SMART; SMO0115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
SQ SEQUENCE 277 AA; 31465 MW; 8749679C30AB46F6 CRC64;

Query Match 19.2%; Score 419; DB 6; Length 277;
Best Local Similarity 33.6%; Pred. No. 3.2e-29;
Matches 92; Conservative 49; Mismatches 91; Indels 42; Gaps 5;

Qy 150 DLAYLSMPEPCGHLIINNVPFCRESGLRTRTGSNIDCEKLRFRFSLHFWVEKGLTAKM 209
Db 34 DSYKMDYFENGGLCIINNNKFNHSTGMPFSRSGTGDVDAANLRETFTNLKYEVRNKDLTR 93
Qy 210 KMWLALLELARQDHGALDCCVVILSHGCOASHLQFPQAVYGTDCGCPVSVEKIVNIFNG 269
Db 94 EQIVALLDSVSRSHKSSFCVLLSHGEE-----GLIYGTNG-PVDLKKLTGFFRG 145
Qy 270 TSCPSLGGKPKLFFIOACGGEKQDHGFVASTSPEDSPGSPNPEPDATPFQGLRTFDQL 329
Db 146 DCCRTLTGKPKLFFIOACRGTELDGCIETDSTGDDM----- 181
Qy 330 DAISLPTSPDIFVSYSTFPFVSWRDPKSGSVVETLDDIFEQWASHEDLSLLLRVAN 389
Db 182 IACQKIPVEADFLYAYSTAGYYSWRNSKDGSWFIQSLCSMLRLYAHLEFNMHLTRVNR 241
Qy 390 AV-----SVKGIY---KQMPGCFNFKLFF 413

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Db 242 KVATEFESFLDSAFHGKQIPCVISMLTKELF 275

RESULT 12
Q8JGM9 PRELIMINARY; PRT; 280 AA.
AC Q8JGM9
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 3-like.
GN CASP3
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Hewitt J.E., Bolland D.J.;
RT "Sequence comparisons of an evolutionary chromosomal breakpoint in
RT human, mouse and pufferfish.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY102865; AAM48291.1;
DR GO; GO:0030693; P:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYME.
DR SMART; SMO0115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02027; CASPASE_P10; 1.
DR PROSITE; PS02028; CASPASE_P20; 1.
SQ SEQUENCE 280 AA; 30538 MW; 4D58912159A37347 CRC64;

Query Match 19.2%; Score 418; DB 13; Length 280;
Best Local Similarity 33.9%; Pred. No. 4e-29;
Matches 92; Conservative 44; Mismatches 91; Indels 44; Gaps 4;

Qy 153 YILSMPEPCGHLIINNVPFCRESGLRTRTGSNIDCEKLRFRFSLHFWVEKGLTAKM 212
Db 43 YSLDFPNMGHCIIINNNKFNHSTGMPFSRSGTGDVDAANLRETFTNLKYEVRNKDQTKQM 102
Qy 213 VLALLELARQDHGALDCCVVILSHGCOASHLQFPQAVYGTDCGCPVSVEKIVNIFNGTSC 272
Db 103 KQLLSAAEEDHSHACASFCVLLSHGDE-----GVFFGTG-SVELKYLTSIFRDRC 154
Qy 273 PSLGGKPKLFFIOACGGEKQDHGFVASTSPEDSPGSPNPEPDATPFQGLRTFDQDAI 332
Db 155 KSLVGRPKLFFIOACRGNDLGGIETDSAD-----SST 188
Qy 333 SLSLPTSPDIFVSYSTFPFVSWRDPKSGSVVETLDDIFEQWASHEDLSLLLRVANYS 392
Db 189 TKIPVEADFLYAFSTAGYYSWRNTTSGSWFMSQLSDAISKYGKELEQLHILTRVNHKA 248
Qy 393 VK-----GIYKMPGCFNFKLFF 413
Db 249 VDFESVSNLPGFDAKKQIPCVISMLTKELF 279

RESULT 13
Q8JG42 PRELIMINARY; PRT; 280 AA.
AC Q8JG42
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 3.

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RESULT 15
Q8MKI5
TD Q8MKI5

GN CASP3.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97311173; PubMed=9166581;
RA Grewal P.K., van Deutekom J.C., Mills K.A., Lemmers R.J.,
RA Mathews K.D., Frants R.R., Hewitt J.E.;
RA "The mouse homolog of FRG1, a candidate gene for FSHD, maps proximal
RT to the myodystrophy mutation on chromosome 8.";
RT Mamm. Genome 8:394-398(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98482568; PubMed=9714712;
RA Grewal P.K., Todd L.C., van der Maarel S., Frants R.R., Hewitt J.E.;
RA "FRG1, a gene in the FSH muscular dystrophy region on human chromosome
RT 4q35, is highly conserved in vertebrates and invertebrates.";
RL Gene 216:13-19(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21303262; PubMed=11410364;
RA Bolland D.J., Hewitt J.E.;
RA "Intron loss in the SART1 genes of Fugu rubripes and Tetraodon
RT nigroviridis";
RL Gene 271:43-49(2001).
RN [4]
RP SEQUENCE FROM N.A.
RA Bolland D.J., van Geel M., Carim Todd L., Grewal P.K., Beck A.F.,
RA van der Maarel M. Sr., Frants R.R., de Jong P.J., Hewitt J.E.;
RA "Sequence Comparisons of an Evolutionary Chromosomal Breakpoint in
RT Human, Mouse and Puffer Fish";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN EMBL; AF042797; AAM43816.1;
DR GO; GO:0030693; F:casepase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE.p10.
DR InterPro; IPR001309; ICE.p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; I.
DR PRINTS; PR00376; ILIACENZYM.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02007; CASPASE_P10; 1.
DR PROSITE; PS02008; CASPASE_P20; 1.
SQ SEQUENCE 280 AA; 30524 MW; 4F2D91245A7EC642 CRC64;

Query Match 18.9%; Score 413; DB 13; Length 280;
Best Local Similarity 33.6%; Pred. No. 1.le-28;
Matches 91; Conservative 44; Mismatches 92; Indels 44; Gaps 4;

QY 153 YILSEPCGHCLIIINNVFCBSGLRTTGSNIDCEKLRFRFSIHFVVEVKGDLTAKM 212
DB 43 YSLDPPNMGHCIIINKNKPRDRGTGNTNGTDDVDAANAMKFLSLGYKVKVNDQTNQM 102
QY 213 VLALLELARODHGALDCCVWVILSHGCASHLQFFGAVYGTGCGVSVSEKIVINIFNGTSC 272
DB 103 KQILLVSAEDHSACAFVCLLSHGDE-----GVFGTDG-SVELKYLTLSPRGDRC 154
QY 273 PSLGKPKLFFTOACGGEQKHGFEVASTSPDESEFGSNPEPDATPFQEGRLTFDQLDAI 332
DB 155 KSLVGKPKLFFIOACRGNLDGGIETDSAAD-----SST 188
QY 333 SSIPTFSDIFVSYSTPFGVSWRDPKSGWYVETLDDIEQWAHSEDLSLLLRVANAVS 392
DB 189 TKIPVEADFLYAFSTAPGYISWNTTSGSWFQSLCDALS KYKELEQLHLTRVNHKVA 248
QY 393 VK-----GIYQMPGCGCFNLRKKLFF 413

393 VK-----GIYKQMPGCFNFKLFF 413

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AC QSMK15;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Caspase-3.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Sano J.;
RT "canine caspase-3 gene.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB085580; BAB92962.1; -.
DR GO; GO:0030893; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
SQ SEQUENCE 277 AA; 31334 MW; 7094C76D868BDAB9 CRC64;

Query Match      18.4%; Score 401; DB 6; Length 277;
Best Local Similarity 32.2%; Pred. No. 1.3e-27;
Matches 88; Conservative 51; Mismatches 92; Indels 42; Gaps 5;

QY 150 DLAYILMEPCGHCLIIINNVCRESGLRTRGNSIDCEKLRFRFSSLHFMVEVKGLTA 209
Db |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
34 DNSYKWDYPEWGLCIINNKNFKSTGMAPRSGTDVDAANLRTEFTNLKYEVRNNDITC 93
QY 210 KMWLALALEARQDHGALDCCVWVILSHGCGASHLQFPGAVYGTGCPVSVKIVNIENG 269
Db |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
94 EEILELMNSVSKEDHSKSSFCVLLSHGDE-----GIIFGTNG-FVDLRKVTGFFRG 145
QY 270 TSCPSLGGKPKLFTIQACGGKQKHGFEVASTPEDESFGSNPEPDATPFQEGLETFDQL 329
Db |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
146 DYCRSLTGCKPKLFTIQACRGTELDGCIETDSGIEDDM----- 182
QY 330 DAISSLPTPSDIFVSYSTFGFVSWRDPKSGSWVETLDDIFEQWAHSEDLQSLLLRVAN 389
Db |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
183 -ACOKIPVEADFLYATAPGYYSWRNSKDGSWFIQSLCAMLKLYAHKLEFPHILTRVNR 241
QY 390 AV-----SVKGIY---KMPGCGNFILRKLKLF 412
Db |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
242 KVATEFESFLDSAFHGKQKIPICIVSMITRELY 274

```

Search completed: August 3, 2004, 09:02:42
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 08:55:11 ; Search time 54 Seconds
(without alignments)
2176.662 Million cell updates/sec

Title: US-09-961-201A-1

Perfect score: 2180

Sequence: 1 MDEADRRLLRRCLRLVSEL.....YKQMGCFNLRKLLFFKTS 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1373613

Minimum DB seq length: 0
Maximum DB seq length: 416

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2180	100.0	416	2 AAW39209	Human ICE
2	2180	100.0	416	4 AAE00606	Human cas
3	2166	99.4	416	6 ADA10646	Human cas
4	2158	99.0	416	6 ADA10674	Human cas
5	2157	98.9	416	2 AAY21723	Amino aci
6	2157	98.9	416	5 ABJ01224	Human cas
7	2153	98.8	416	4 AAG67375	Amino aci
8	2153	98.8	416	4 AAU08315	Human asp
9	2153	98.8	416	4 AAE08938	Mammalian
10	2153	98.8	416	4 AAB84374	Amino aci
11	2153	98.8	416	6 ABB82738	Human cas
12	2153	98.8	416	8 ADE52020	Human mam
13	2150	98.6	416	6 ADA10675	Human cas
14	2144	98.3	416	6 ADA10676	Human cas
15	2069.5	94.9	401	6 ADA10677	Human cas
16	1288	59.1	266	4 AAE00620	Human cas
17	1083	49.7	203	2 AAW39208	Human ICE
18	468	21.5	93	5 ABJ04760	Human cas
19	420	19.3	277	4 AAG78712	Pig caspa
20	418	19.2	249	3 AAE26763	Human cas
21	418	19.2	277	2 AAW00372	Apopain C
22	418	19.2	277	2 AAW16600	Apopain C
23	418	19.2	277	2 AAR95831	Human int
24	418	19.2	277	2 AAW00677	Pro-Yama.
25	418	19.2	277	2 AAW41688	Amino aci

26	418	19.2	277	2 AAY21717	Amino aci
27	418	19.2	277	4 AAU05394	Human cas
28	418	19.2	277	4 AAU05395	Mouse cas
29	418	19.2	277	4 AAE00600	Human cas
30	418	19.2	277	5 ABG30904	Human mem
31	418	19.2	277	5 AAQ01218	Human cas
32	418	19.2	277	6 AAQ019867	Bacteriop
33	418	19.2	277	7 ADD25641	Binding d
34	418	19.2	277	7 ADE63082	Human Pro
35	416.5	19.1	245	4 AAB59579	Human cas
36	414.5	19.0	261	4 AAE00610	Chimeric
37	414	19.0	241	4 AAB98654	Caspase-3
38	409	18.8	277	2 AAW47089	Rat inter
39	409	18.8	277	7 ADE63080	Rat Prote
40	408	18.7	277	2 AAW48937	Mutant hu
41	408	18.7	277	2 AAW48937	Mutant hu
42	378	17.3	286	3 AAY56997	Human pro
43	378	17.3	286	4 AAB59578	Human cas
44	374	17.2	254	4 AAB98656	Caspase-8
45	361.5	16.6	244	4 AAB98655	Caspase-7

ALIGNMENTS

RESULT 1
AAW39209
ID AAW39209 standard; peptide; 416 AA.
XX
AC AAW39209;
XX
XX
DT 18-MAY-1998 (first entry)
XX
DE Human ICE LAP-6 polypeptide.
XX
KW ICE LAP-6; interleukin-1 beta converting enzyme apoptosis protease-6;
KW viral infection; tumour; inflammation; osteoporosis; AIDS; human;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
FN EP080904-A2.
XX
PD 26-NOV-1997.
XX
PF 19-MAY-1997; 97EP-00303397.
XX
PR 20-MAY-1996; 96US-0017949P.
PR 23-MAY-1996; 96US-0020344P.
PR 05-JUN-1996; 96US-0018961P.
XX
PA (SMK) SMITHKLINE BEECHAM CORP.
PA (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI) UNIV MICHIGAN.
PI Dixit VM, He W, Ruben SM, Kikly KK;
XX WPI; 1998-001790/01.
DR N-PSDB; AAV03401.
XX
XX
PT DNA encoding interleukin-1 beta converting enzyme apoptosis protease-6 -
PT useful to develop products to treat, e.g. viral infection, tumour,
XX Alzheimer's disease, inflammation, osteoporosis and AIDS.
PS Claim 4; Fig 1; 44pp; English.
XX
CC This is a human interleukin-1 beta converting enzyme apoptosis protease-6
CC (ICE LAP-6) polypeptide. The ICE LAP-6 polypeptide and agonists to the
CC polypeptide can be used to induce apoptosis, e.g. as an antiviral or
CC antitumour agent, control embryonic development and tissue homeostasis
CC and the roles of such factors in dysfunction and disease. Antagonists
CC which inhibit the activity of the ICE LAP-6 polypeptide can be used to
CC treat, Alzheimer's or Parkinson's disease, rheumatoid arthritis, septic

CC shock, sepsis, stroke, chronic, acute or central nervous system
 CC inflammation, osteoporosis, ischaemia reperfusion injury, cell death
 CC associated with cardiovascular disease, polycystic kidney disease,
 CC apoptosis of endothelial cells in cardiovascular disease, degenerative
 CC liver disease, multiple sclerosis, cerebellar degeneration, ischaemic
 CC injury, myocardial infarction, acquired immunodeficiency syndrome (AIDS),
 CC myelodysplastic syndrome, aplastic anaemia, male pattern baldness and
 CC head injury damage. They can also be used for detection and diagnosis
 XX
 SQ Sequence 416 AA;

Query Match 100.0%; Score 2180; DB 2; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1e-219; Indels 0; Gaps 0;
 Matches 416; Conservative 0; Mismatches 0;

QY 1 MDEADRLRLRCLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
 DB 1 MDEADRLRLRCLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
 QY 61 DLETRGSQALPLFISCLDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLPRPKPEV 120
 DB 61 DLETRGSQALPLFISCLDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLPRPKPEV 120
 QY 121 LRPEPRPVVDIGSGGFDVGALSLRGNDLAVILSMPECGHCLIIINNVCRESGLRTR 180
 DB 121 LRPEPRPVVDIGSGGFDVGALSLRGNDLAVILSMPECGHCLIIINNVCRESGLRTR 180
 QY 181 TGSNIDCEKLRFRFSSLHFVVEVKGDLTAKKMWLALLELARQDHGALDCVVVILSHGQ 240
 DB 181 TGSNIDCEKLRFRFSSLHFVVEVKGDLTAKKMWLALLELARQDHGALDCVVVILSHGQ 240
 QY 241 ASHLQPPGAVYGTGDCPVSVKEKIVNIPNGTSCPSLGGKPKLFTIQACGGKQKHGEFVAS 300
 DB 241 ASHLQPPGAVYGTGDCPVSVKEKIVNIPNGTSCPSLGGKPKLFTIQACGGKQKHGEFVAS 300
 QY 301 TSPEDSPGSPNPEPDATPQEGRLTDFDQDAISLTPSPDIFVSYSTFPGFVSWRDPKSG 360
 DB 301 TSPEDSPGSPNPEPDATPQEGRLTDFDQDAISLTPSPDIFVSYSTFPGFVSWRDPKSG 360
 QY 361 SWYVETLDDIFEQWAHSEDQLSLLRVANAVSVKGIYKQMPGCFNLRKLPKFTS 416
 DB 361 SWYVETLDDIFEQWAHSEDQLSLLRVANAVSVKGIYKQMPGCFNLRKLPKFTS 416

RESULT 2

AAE00606
 ID AAE00606 standard; protein; 416 AA.

AC AAE00606;

XX 02-JUL-2001 (first entry)

DT Human caspase-9, alternative version.

DE Human; caspase-9; interleukin-1 converting enzyme; ICE-LAP6; Mch6;
 XX cysteine protease; apoptosis; caspase expression cassette; metastasis;
 KW tumour; cathepsin B; urokinase; proliferation; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

PH Misc-difference 28 /note= "Encoded by GCC; Ala is present in the sequence
 FT shown in page 105-107 (AAE00620) "

FT Misc-difference 96 /note= "Encoded by GCA; Ala is present in the sequence
 FT shown in page 105-107 (AAE00620) "

FT Misc-difference 139..290 /note= "Encoded by GTCGAG; Amino acid residues from
 FT position 140 to 289 present in this sequence are not
 FT found in the sequence shown in page 105-107 (AAE00620) "

FT Cleavage-site 315..316 /label= Proteolytic_cleavage_site

FT Cleavage-site 330..331
 FT /label= Proteolytic_cleavage_site

XX WO200129232-A2.

XX 26-APR-2001.

XX 19-OCT-2000; 2000WO-US028941.

XX 20-OCT-1999; 99US-0160559P.

XX 14-AUG-2000; 2000US-0225564P.

XX (SCIO-) SCIOS INC.

XX Cordell B, Li Y;

XX WPI; 2001-290920/30.

XX N-PSDB; AAD03916.

XX Novel fusion polypeptide comprising first and second caspase subunit
 PT separated by cleavage site not associated in nature with caspase subunit,
 PT useful for cloning gene encoding enzymes involved in proteolytic
 PT cleavage.

XX Claim 4; Fig 18; 116pp; English.

XX The present sequence is an alternative version of human Caspase-9 also
 CC known as interleukin-1 converting enzyme (ICE) LAP6 and Mch6. Caspases
 CC are a family of cysteine proteases, that participate in the initiation
 CC and execution of apoptosis. Caspases exist as pro-enzymes, activated by
 CC cleavage into a large and small subunit, occurring after specific
 CC aspartic acid residues within the pro-enzyme sequence. The present
 CC invention relates to a method for functional cloning of genes encoding
 CC proteins or enzymes involved in proteolytic cleavage. The invention is
 CC based on the use of caspase expression cassettes comprising the coding
 CC sequence of a proteolytic cleavage site flanked by sequences encoding two
 CC caspase subunits. A fusion polypeptide comprising a first and a second
 CC caspase subunit, separated by a cleavage site not associated in nature,
 CC is useful for cloning gene encoding enzymes involved in proteolytic
 CC cleavage. An expression cassette containing fusion polypeptide is used to
 CC identify a mutant cell line deficient in an enzyme of interest and is
 CC also useful for diagnosis and suppression of proliferation or metastases
 CC of a tumour cell characterised by overexpression of a polypeptide (e.g.
 CC Cathepsin B or urokinase, selectively expressed in the tumour cells). DNA
 CC encoding fusion polypeptide is used in gene therapy. Note: This sequence
 CC SEQ.ID.NO.18 is stated as being the same as that shown in page 105-107
 CC (See AAE00620) in the specification. However these sequences differ at
 CC several positions
 XX
 SQ Sequence 416 AA;

Query Match 100.0%; Score 2180; DB 4; Length 416;

Best Local Similarity 100.0%; Pred. No. 1e-219; Indels 0; Gaps 0;
 Matches 416; Conservative 0; Mismatches 0;

QY 1 MDEADRLRLRCLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

DB 1 MDEADRLRLRCLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

QY 61 DLETRGSQALPLFISCLDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLPRPKPEV 120

DB 61 DLETRGSQALPLFISCLDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLPRPKPEV 120

QY 121 LRPEPRPVVDIGSGGFDVGALSLRGNDLAVILSMPECGHCLIIINNVCRESGLRTR 180

DB 121 LRPEPRPVVDIGSGGFDVGALSLRGNDLAVILSMPECGHCLIIINNVCRESGLRTR 180

QY 181 TGSNIDCEKLRFRFSSLHFVVEVKGDLTAKKMWLALLELARQDHGALDCVVVILSHGQ 240

DB 181 TGSNIDCEKLRFRFSSLHFVVEVKGDLTAKKMWLALLELARQDHGALDCVVVILSHGQ 240

QY 241 ASHLQPPGAVYGTGDCPVSVKEKIVNIPNGTSCPSLGGKPKLFTIQACGGKQKHGEFVAS 300

DB 241 ASHLQPPGAVYGTGDCPVSVKEKIVNIPNGTSCPSLGGKPKLFTIQACGGKQKHGEFVAS 300

Db 241 ASHLQFPGAVYGTGCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300
 QY 301 TSPEDSGSNPEPDATPFQGLRTFDQDAISSLPTSDIFVSYSTFGFVSWRDPKSG 360
 Db 301 TSPEDSGSNPEPDATPFQGLRTFDQDAISSLPTSDIFVSYSTFGFVSWRDPKSG 360
 QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLFKFTS 416
 Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLFKFTS 416

RESULT 3 ADA10674

ID ADA10646 standard; protein; 416 AA.

XX ADA10646;

DT 06-NOV-2003 (first entry)

XX Human caspase-9 protein.

XX Human; caspase-9; anti-HIV; neurotropic; neuroprotective; vasotropic;
 KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease.

XX Homo sapiens.

OS
 XX
 XX US2002160975-A1.

XX 31-OCT-2002.

XX 06-FEB-2002; 2002US-00068569.

XX 08-FEB-2001; 2001US-0267966P.

PR 24-AUG-2001; 2001US-00939293.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;

PI WPI; 2003-219992/21.

DR N-PSDB; ADA10661.

XX New nucleic acid molecules encoding a peptide or polypeptide that binds
 PT to a portion of an inhibitor of apoptosis protein, useful for inducing
 PT apoptosis and identifying inhibitors or enhancers of apoptosis for
 PT treating AIDS, or cancer.

XX Claim 36; Page 25-26; 52pp; English.

PS The invention relates to an isolated nucleic acid molecule comprising a
 CC polynucleotide that encodes a polypeptide or peptide, or its variants
 CC that specifically binds to at least a portion of an inhibitor of
 CC apoptosis protein (IAP). Also included are a peptide or a polypeptide
 CC comprising at least an N terminus sequence of caspase-9 N-terminal
 CC linker sequence, a first portion of a procaspase-9 that specifically
 CC binds at least a portion of an IAP and a second portion of a procaspase-9
 CC containing a mutated active site, where the peptide or polypeptide
 CC specifically binds at least a portion of an IAP and lacks cysteine
 CC protease activity, and at least a portion of caspase-3, where the peptide
 CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
 CC an IAP or an IAP Bir3 domain) or at least a portion of a mutated
 CC procaspase-9, which fails to undergo normal processing and possesses wild
 CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
 CC polynucleotide sequence that encodes the caspase-9 N-terminal linker), an
 CC expression vector comprising any of the nucleic acids, a host cell
 CC containing the expression vector, an antibody that specifically binds to
 CC the peptide or polypeptide, an antibody that specifically binds to an
 CC epitope located on the N-terminus of a caspase-9-pl2, inducing apoptosis
 CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
 CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,

CC identifying a compound that inhibits the peptide or polypeptide,
 CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
 CC a process for the manufacture of a compound for inhibiting or enhancing
 CC apoptosis in a cell. The nucleic acid molecules and peptides or
 CC polypeptides are useful for inducing apoptosis and identifying inhibitors
 CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
 CC ischaemic injury, cancer, autoimmune diseases. The present sequence
 CC represents the full length caspase-9 protein.

XX Sequence 416 AA;

Query Match 99.4%; Score 2166; DB 6; Length 416;

Best Local Similarity 99.3%; Pred. No. 3e-218; 2; Indels 0; Gaps 0;

Matches 413; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVELEQDQLMDVLLSRELFPHMIEDIQAGSGSRDQARQLII 60

Db 1 MDEADRLRLRCRLRLVELEQDQLMDVLLSRELFPHMIEDIQAGSGSRDQARQLII 60

QY 61 DLETRGSQALPLFISCLDTGQDMLASFLRTNRQAKLSKPTLENLTPVLRPEIRKPEV 120

Db 61 DLETRGSQALPLFISCLDTGQDMLASFLRTNRQAKLSKPTLENLTPVLRPEIRKPEV 120

QY 121 LRPEPRPVYDGGGPDVGALESRLGNADLAYILSMFPGHCLIIINNVCRESGLRTR 180

Db 121 LRPEPRPVYDGGGPDVGALESRLGNADLAYILSMFPGHCLIIINNVCRESGLRTR 180

QY 181 TGSNIDCEKLRFRFSLHFVMEVKGDLTAKQWLALLELARQDHGALDCCVVILSHGQC 240

Db 181 TGSNIDCEKLRFRFSLHFVMEVKGDLTAKQWLALLELARQDHGALDCCVVILSHGQC 240

QY 241 ASHLQFPGAVYGTGCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300

Db 241 ASHLQFPGAVYGTGCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVAS 300

QY 301 TSPEDSGSNPEPDATPFQGLRTFDQDAISSLPTSDIFVSYSTFGFVSWRDPKSG 360

Db 301 TSPEDSGSNPEPDATPFQGLRTFDQDAISSLPTSDIFVSYSTFGFVSWRDPKSG 360

QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLFKFTS 416

Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLFKFTS 416

RESULT 4

ADA10674

ID ADA10674 standard; protein; 416 AA.

XX ADA10674;

XX 06-NOV-2003 (first entry)

XX Human caspase-9 protein D315A mutant.

XX Human; caspase-9; anti-HIV; neurotropic; neuroprotective; vasotropic;
 KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease; mutant; mutein.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 315 /note= "Wild-type Asp substituted by Ala"

XX US2002160975-A1.

XX 31-OCT-2002.

XX 06-FEB-2002; 2002US-00068569.

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PR 08-FEB-2001; 2001US-0267966P.
PR 24-AUG-2001; 2001US-00939293.
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX Alnemri ES;
PI WPI; 2003-219992/21.
XX
DR New nucleic acid molecules encoding a peptide or polypeptide that binds
PT to a portion of an inhibitor of apoptosis protein, useful for inducing
PT apoptosis and identifying inhibitors or enhancers of apoptosis for
PT treating AIDS, or cancer.
XX
PS Claim 36; Page; 52pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule comprising a
CC polynucleotide that encodes a polypeptide or peptide, or its variants
CC that specifically binds to at least a portion of an inhibitor of
CC apoptosis protein (IAP). Also included are a peptide or a polypeptide
CC (comprising at least an N terminus sequence of caspase-9 N-terminal
CC linker sequence, a first portion of a procaspase-9 that specifically
CC binds at least a portion of an IAP and a second portion of a procaspase-9
CC containing a mutated active site, where the peptide or polypeptide
CC specifically binds at least a portion of an IAP and lacks cysteine
CC protease activity, and at least a portion of caspase-3, where the peptide
CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
CC an IAP or an IAP Bir3 domain) or at least a portion of a mutated
CC procaspase-9, which fails to undergo normal processing and possesses wild
CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
CC polynucleotide sequence that encodes the caspase-9 N-terminal linker), an
CC expression vector comprising any of the nucleic acids, a host cell
CC containing the expression vector, an antibody that specifically binds to
CC the peptide or polypeptide, an antibody that specifically binds to an
CC epitope located on the N-terminus of a caspase-9-pl2, inducing apoptosis
CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
CC identifying a compound that inhibits the peptide or polypeptide,
CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
CC a process for the manufacture of a compound for inhibiting or enhancing
CC apoptosis in a cell. The nucleic acid molecules and peptides or
CC polypeptides are useful for inducing apoptosis and identifying inhibitors
CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
CC ischaemic injury, cancer, autoimmune diseases. The present sequence
CC represents the caspase-9 protein mutated to ablate the autocatalytic
CC cleavage site in the linker region. Note: the present sequence is not
CC shown in the specification but was created by the indexer using the
CC information in the claims and the wild type caspase-9 sequence.
XX
SQ Sequence 416 AA;
Query Match 99.0%; Score 2158; DB 6; Length 416;
Best Local Similarity 99.0%; Pred. No. 2.1e-217;
Matches 412; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MDEADRLRLRCLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
QY 61 DLTRGSQLPLFTSCLEDTGQDMLASFRTNRQAGKLSKPTLENLTPVVLREIRKPEV 120
Db 61 DLTRGSQLPLFTSCLEDTGQDMLASFRTNRQAGKLSKPTLENLTPVVLREIRKPEV 120
QY 121 LRPEFRPVDIGGGFGDVGALSLRGNADLAVILSMPCGHCLIIINNWNFCRESGLRTR 180
Db 121 LRPEFRPVDIGGGFGDVGALSLRGNADLAVILSMPCGHCLIIINNWNFCRESGLRTR 180
QY 181 TGSNIDCEKLRRFSSHFVVEVKGDLTAKKMWLALLELARQDHGALDCCVVILSHGCQ 240
Db 181 TGSNIDCEKLRRFSSHFVVEVKGDLTAKKMWLALLELARQDHGALDCCVVILSHGCQ 240
QY 241 ASHLQFPGAVYTGDCPVSVKEKIVNIENGTSCPSLGKPKLFFIOACGGEQKDHGEVAS 300

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Db 241 ASHLQFPGAVYTGDCPVSVKEKIVNIENGTSCPSLGKPKLFFIOACGGEQKDHGEVAS 300
QY 301 TSPDESPGNSNPEDATPFQGLRFTDQDAISSLPTSDIFVSVYSTPFGFVSWRDPKSG 360
Db 301 TSPDESPGNSNPEDATPFQGLRFTDQDAISSLPTSDIFVSVYSTPFGFVSWRDPKSG 360
QY 361 SWIVETLDDIIEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCCNFLEKPLFFKTS 416
Db 361 SWIVETLDDIIEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCCNFLEKPLFFKTS 416
RESULT 5
AAAY21723
ID AAY21723 standard; protein; 416 AA.
XX
AC AAY21723;
DT 10-SEP-1999 (first entry)
XX
DE Amino acid sequence of caspase-9 (ICE-LAP6).
XX
KW Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
KW autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
KW tumour cell; myocardial infarction; human.
XX
OS Homo sapiens.
XX
FN WO9935277-A2.
XX
PD 15-JUL-1999.
XX
PF 11-JAN-1999; 99WO-US000632.
XX
PR 09-JAN-1998; 98US-0070987P.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Alnemri ES;
XX
DR WPI; 1999-419353/35.
DR N-PSDB; AAX81225.
XX
PT New isolated nucleic acid molecule encoding a rev-caspase - used for
PT screening and identifying inhibitors or enhancers for treating cancer or
PT autoimmune disease.
XX
PS Disclosure; Fig 19A-B; 74pp; English.
XX
CC The invention relates to nucleic acid molecules encoding rev-caspases.
CC Rev-caspases are cysteine proteases that specifically cleave proteins
CC after Asp residues and is expressed as a zymogen, in which the small
CC subunit is N-terminal to a large subunit. A gene delivery vehicle
CC comprising a rev-caspase coding sequence is useful for the treatment of
CC cancer, where the gene delivery vehicle is internalised by tumour cells.
CC The gene delivery vehicle can also be used to treat autoimmune diseases.
CC Cells transfected with a rev-caspase expressing vector can be used in
CC identification of inhibitors or enhancers of caspase-mediated apoptosis.
CC In vitro translated rev-caspase can be used to identify an inhibitor or
CC enhancer of caspase processing activity. Caspase inhibitors are useful
CC for treating neurodegenerative diseases as well as for inhibiting
CC apoptosis in the heart following myocardial infarction. Sequences
CC AAX81217 -AAX81226 represent human caspase genes encoding caspase 1-10
CC gene products (AAV21715-Y21724)
XX
SQ Sequence 416 AA;
Query Match 98.9%; Score 2157; DB 2; Length 416;
Best Local Similarity 99.0%; Pred. No. 2.6e-217;
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 MDEADRLRLRCLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

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QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRNRQAGKLSKPTLENLTVPVLRPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLDGTQDMLASFLRNRQAGKLSKPTLENLTVPVLRPEIRKPEV 120
QY 121 LRPETPRVDITGSGGFGDVGALESIRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180
Db 121 LRPETPRVDITGSGGFGDVGALESIRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRRRFSSLFHFMVEVKGDLTAKKMWLALLELARDHGALDCCVVVILSHGCG 240
Db 181 TGSNIDCEKLRRRFSSLFHFMVEVKGDLTAKKMWLALLELARDHGALDCCVVVILSHGCG 240
QY 241 ASHLQFPGAVGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIQAACGGEQKDHGFEVAS 300
Db 241 ASHLQFPGAVGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIQAACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLAISLPTPSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLAISLPTPSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIPEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416
Db 361 SWYVETLDDIPEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416
```

```
RESULT 6
ABJ01224
ID ABJ01224 standard; protein; 416 AA.
XX AC ABJ01224;
DT 18-SEP-2002 (first entry)
DE Human caspase-9 SEQ ID NO: 30.
XX KW Human; caspase; rev-caspase; gene therapy; protease; apoptosis; cancer;
KW autoimmune disease; cytostatic; immunosuppressive.
XX OS Homo sapiens.
XX FN US6376226-B1.
XX PD 23-APR-2002.
XX PF 26-APR-2000; 2000US-00561756.
XX PR 09-JAN-1998; 98US-0070897P.
XX PR 08-JAN-1999; 99US-00227721.
XX PA (UYJE-) UNIV JEFFERSON THOMAS.
XX PI Alnemri ES;
XX WPI; 2002-453146/48.
XX DR N-PSDB; ABT03972.
```

New rev-caspases engineered to contain the small subunit fused in frame N-terminal to the large subunit, which is in reverse order to the wild type caspases, are useful to treat cancer and autoimmune diseases.

XX PS Disclosure; Fig 19; 81pp; English.

XX CC The present invention provides the protein and coding sequences of human rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences can be used in the gene therapy of cancer and autoimmune diseases. The present sequence is a protein described in the exemplification of the invention

XX SQ Sequence 416 AA;

Query Match 98.9%; Score 2157; DB 5; Length 416;
Best Local Similarity 99.0%; Pred. No. 2.6e-217;

```
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFPRPHMIEDIQRAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFPRPHMIEDIQRAGSGRRDQARQLII 60
QY 61 DLETRGSQALPLFISCLDGTQDMLASFLRNRQAGKLSKPTLENLTVPVLRPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLDGTQDMLASFLRNRQAGKLSKPTLENLTVPVLRPEIRKPEV 120
QY 121 LRPETPRVDITGSGGFGDVGALESIRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180
Db 121 LRPETPRVDITGSGGFGDVGALESIRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRRRFSSLFHFMVEVKGDLTAKKMWLALLELARDHGALDCCVVVILSHGCG 240
Db 181 TGSNIDCEKLRRRFSSLFHFMVEVKGDLTAKKMWLALLELARDHGALDCCVVVILSHGCG 240
QY 241 ASHLQFPGAVGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIQAACGGEQKDHGFEVAS 300
Db 241 ASHLQFPGAVGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIQAACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLAISLPTPSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLAISLPTPSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIPEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416
Db 361 SWYVETLDDIPEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416
```

RESULT 7

AAG67375
ID AAG67375 standard; protein; 416 AA.

XX AC AAG67375;

DT 13-NOV-2001 (first entry)

DE Amino acid sequence of human Mch6 polypeptide.

XX KW Mch6; ced-3 homologue; ICE; interleukin-1-beta converting enzyme;
KW aspartate-specific cysteine protease; ASCP; apoptotic cell death;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW retinitis pigmentosa; cerebellar degeneration; myelodysplastic syndrome;
KW aplastic anemia; ischemic injury; myocardial infarction; stroke; cancer;
KW reperfusion injury; autoimmune disease; systemic lupus erythematosus;
KW immune-mediated glomerulonephritis; viral infection; cell death.

XX OS Homo sapiens.

XX PN US6274318-B1.

XX PD 14-AUG-2001.

XX PF 13-MAY-1999; 99US-00311760.

XX PR 29-MAY-1997; 97US-00865579.

XX PA (UYJE-) UNIV JEFFERSON THOMAS.

XX PI Alnemri ES, Fernandes-Alnemri T, Litwack G;

XX DR WPI; 2001-540372/60.

XX DR N-PSDB; AAH77927.

XX PT Identifying mammalian homolog ced-3 homolog (Mch)6 activity modulators, useful for treating lymphomas, carcinomas and hormone dependent tumors, PT Alzheimer's disease, Parkinson's disease, comprises using Mch6 polypeptide.

XX PS Example 1; Fig 1a-c; 36pp; English.

CC The present sequence represents a human Mch6 polypeptide. Mch6 is a ced-3
 CC homologue, and is a member of the ICE (interleukin-1-beta converting
 CC enzyme) family of aspartate-specific cysteine proteases (ASCPs). The
 CC specification describes a method for identifying mammalian Mch6 activity
 CC modulators (inhibitors or enhancers). The compounds identified by the
 CC method are useful as pharmaceuticals for treating or preventing diseases
 CC characterized by increased apoptotic cell death such as Alzheimer's
 CC disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis
 CC pigmentosa, or cerebellar degeneration, myelodysplastic syndromes such as
 CC aplastic anemia, ischemic injury including myocardial infarction, stroke
 CC and reperfusion injury. The compounds are also useful for treating
 CC diseases characterized by loss of apoptotic cell death such as cancers,
 CC e.g. lymphomas, carcinomas and hormone dependent tumours such as breast,
 CC prostate and ovarian cancer. Increased cell survival or apoptosis
 CC inhibition also results in autoimmune diseases such as systemic lupus
 CC erythematosus and immune-mediated glomerulonephritis as well as viral
 CC infections such as herpes virus, pox virus and adenovirus and the novel
 CC identified compounds are useful for treating these conditions. The Mch6
 CC inhibitors are used to treat or to reduce severity of diseases
 CC characterized by increased programmed cell death
 XX
 CC Sequence 416 AA;

Query Match 98.8%; Score 2153; DB 4; Length 416;
 Best Local Similarity 98.8%; Pred. No. 6.9e-217;
 Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDLQDMLASFLRTNQAGKLSKPTLENTPVVLRPEIRKPEV 60
 DB 1 MDEADRLRLRCRLRLVEELQVDLQDMLASFLRTNQAGKLSKPTLENTPVVLRPEIRKPEV 60
 QY 61 DLETGSGQALPLFISCLEDTGQDMLASFLRTNQAGKLSKPTLENTPVVLRPEIRKPEV 120
 DB 61 DLETGSGQALPLFISCLEDTGQDMLASFLRTNQAGKLSKPTLENTPVVLRPEIRKPEV 120
 QY 121 LRPEPRPVVDIGSGGFGDVGALSLRGNADLAYILSMPCGHCILINNVCRESGLRTR 180
 DB 121 LRPEPRPVVDIGSGGFGDVGALSLRGNADLAYILSMPCGHCILINNVCRESGLRTR 180
 QY 181 TGSNIDCEKLRFRFSSILHFVVEKGDITAKKMWLALLELARODHGALDCVWVILSHGQ 240
 DB 181 TGSNIDCEKLRFRFSSILHFVVEKGDITAKKMWLALLELARODHGALDCVWVILSHGQ 240
 QY 241 ASHLQFPAGVYGTGCPVSEKIVNIFNGTSCPSLGKPKLFFIQACGGKQKHGEVAS 300
 DB 241 ASHLQFPAGVYGTGCPVSEKIVNIFNGTSCPSLGKPKLFFIQACGGKQKHGEVAS 300
 QY 301 TSPEDSPGSGNPPDPATPFOEGLRTDQDAISSLPTPSDIFVSYSTFPGFVSWRDPKSG 360
 DB 301 TSPEDSPGSGNPPDPATPFOEGLRTDQDAISSLPTPSDIFVSYSTFPGFVSWRDPKSG 360
 QY 361 SWYVETLDDIFFEQWAHSEDLQSLLRVANAVSVKGIYKOMPCCGFNLRKLPFKTS 416
 DB 361 SWYVETLDDIFFEQWAHSEDLQSLLRVANAVSVKGIYKOMPCCGFNLRKLPFKTS 416

RESULT 8
 AAU08315
 ID AAU08315 standard; protein; 416 AA.

XX AAU08315;
 AC AAU08315;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 DE Human aspartate-specific cysteine protease, MCH6.
 XX
 KW Human; aspartate-specific cysteine protease; MCH6; neutropic;
 KW neuroprotective; anti-Parkinsonian; antianemic; vasotropic; cardiant;
 KW cerebroprotective; mammalian ced-3 homologue 6; gene therapy; apoptosis;
 KW Alzheimer's disease; Parkinson's disease; retinitis pigmentosa;
 KW cerebellar degeneration; myelodysplastic syndrome; aplastic anaemia;
 KW ischaemic injury; myocardial infarction; stroke; reperfusion injury;
 KW amyotrophic lateral sclerosis.

XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Active-site 285..289
 FT Cleavage-site 312..316
 FT /label= Granzyme_beta_cleavage_site
 FT /note= "Cleavage occurs after Asp at position 315"
 FT Cleavage-site 327..331
 FT /label= Granzyme_beta_cleavage_site
 FT /note= "Cleavage occurs after Asp at position 330"
 XX
 US2001016345-A1.
 XX 23-AUG-2001.
 XX 22-DEC-2000; 2000US-00746731.
 XX 29-MAY-1997; 97US-00865579.
 PR 25-FEB-1999; 99US-00257218.
 XX
 XX (ALNE/) ALNEMRI E S.
 PA (FERN/) FERNANDES-ALNEMRI T.
 PA (LITW/) LITWACK G.
 PI Alnemri ES, Fernandes-Alnemri T, Litwack G;
 XX
 DR WPI; 2001-535542/59.
 DR N-PSDB; AAS12629.
 XX
 PT New Mch6 polypeptides and genes encoding the polypeptides useful for
 PT diagnosing, treating or reducing the severity of cell death-mediated
 PT diseases such as neurodegenerative diseases e.g. Alzheimer's disease,
 PT Parkinson's disease.
 XX
 PS Claim 8; Fig 1; 15pp; English.
 XX
 CC The invention relates to an isolated gene encoding MCH6 (mammalian ced-3
 CC homologue 6) an aspartate-specific cysteine protease and the MCH6
 CC polypeptide. The MCH6-encoding nucleic acids and polypeptides can be used
 CC to diagnose, treat (e.g. by gene therapy) or reduce the severity of cell
 CC death-mediated diseases (i.e. apoptotic) such as neurodegenerative
 CC diseases e.g. Alzheimer's disease, Parkinson's disease, amyotrophic
 CC lateral sclerosis, retinitis pigmentosa and cerebellar degeneration, and
 CC myelodysplastic syndromes, e.g. aplastic anaemia, ischaemic injury,
 CC myocardial infarction, stroke and reperfusion injury. The MCH6-encoding
 CC nucleic acids and polypeptides can also be used to diagnose or generate
 CC reagents to diagnose diseases mediated or characterised by programmed
 CC cell death. A purified recombinant MCH6 protein can be used to measure
 CC hydrolysis rates for various substrates such as DEVD-AMC and YVAD-AMC in
 CC a continuous fluorometric assay. The present sequence represents human
 CC MCH6
 XX
 XX Sequence 416 AA;

Query Match 98.8%; Score 2153; DB 4; Length 416;
 Best Local Similarity 98.8%; Pred. No. 6.9e-217;
 Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MDEADRLRLRCRLRLVEELQVDLQDMLASFLRTNQAGKLSKPTLENTPVVLRPEIRKPEV 60
 DB 1 MDEADRLRLRCRLRLVEELQVDLQDMLASFLRTNQAGKLSKPTLENTPVVLRPEIRKPEV 60
 QY 61 DLETGSGQALPLFISCLEDTGQDMLASFLRTNQAGKLSKPTLENTPVVLRPEIRKPEV 120
 DB 61 DLETGSGQALPLFISCLEDTGQDMLASFLRTNQAGKLSKPTLENTPVVLRPEIRKPEV 120
 QY 121 LRPEPRPVVDIGSGGFGDVGALSLRGNADLAYILSMPCGHCILINNVCRESGLRTR 180
 DB 121 LRPEPRPVVDIGSGGFGDVGALSLRGNADLAYILSMPCGHCILINNVCRESGLRTR 180
 QY 181 TGSNIDCEKLRFRFSSILHFVVEKGDITAKKMWLALLELARODHGALDCVWVILSHGQ 240
 DB 181 TGSNIDCEKLRFRFSSILHFVVEKGDITAKKMWLALLELARODHGALDCVWVILSHGQ 240

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Db 181 TGSNIDCEKLRRRSSPHFMVEVKGDLTAKKMWLALLELAQQDHGALDCCVVVILSHGQC 240
QY 241 ASHLQFPGAVYGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
Db 241 ASHLQFPGAVYGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQGLRTFDQDLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQGLRTFDQDLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 9
AAE08938
ID AAE08938 standard; protein; 416 AA.
XX
AC AAE08938;
XX
DT 15-NOV-2001 (first entry)
XX
DE Mammalian ced-3 homologue 6 (Mch6).
XX
KW Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer;
KW aspartate-specific cysteine protease; ASCP; apoptosis; therapy;
KW autoimmune disease; cerebellar degeneration; Alzheimer's disease;
KW cytostatic; Parkinson's disease; immunomodulator; antimicrobial;
KW viral infection; cell death-mediated disease; neuroprotective.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Active-site 285..290 /note="Active site pentapeptide"
FT Cleavage-site 315..316
FT Cleavage-site 330..331
XX
PN US6271361-B1.
XX
PD 07-AUG-2001.
XX
PF 25-FEB-1999; 99US-00257218.
XX
PR 29-MAY-1997; 97US-00865579.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Alnemri ES, Fernandes-Alnemri T, Litwack G;
XX
DR WPI; 2001-528686/58.
XX
DR N-PSDB; AAD15656.
XX
PT New apoptotic genes and their apoptotic protease products, useful for
PT modulating apoptosis for the therapeutic treatment of human diseases,
PT e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's
PT disease.
XX
PS Claim 2; Fig 1; 36pp; English.
XX
CC The invention relates to an isolated gene encoding apoptic protease,
CC mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the aspartate-
CC specific cysteine protease (ASCP) family. Mch6 DNA and protein sequences
CC are useful for modulating apoptosis for the therapeutic treatment of
CC human diseases. Mch6 sequences are useful for upregulating apoptosis
CC (e.g. for treating cancers, autoimmune disease or viral infections) or
CC downregulating apoptosis (e.g. for treating Alzheimer's disease,
CC Parkinson's disease or cerebellar degeneration). The Mch6 sequence is
CC useful for diagnosing, treating or reducing the severity of cell death-
CC mediated diseases, as well as other diseases mediated by either increased
CC or decreased programmed cell death. The present amino acid sequence is
CC Mch6
```

```
XX SQ Sequence 416 AA;
Query Match
Best Local Similarity 98.8%; Score 2153; DB 4; Length 416;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSRELFRPHMIEDIQAGSGSRDDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLMDVLLSSELFRPHMIEDIQAGSGSRDDQARQLII 60
QY 61 DLETRGSQALPLFTISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVWLPEIRKPEV 120
Db 61 DLETRGSQALPLFTISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVWLPEIRKPEV 120
QY 121 LRPTPRVDIGSGGFGDVGALESIRGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
Db 121 LRPTPRVDIGSGGFGDVGALESIRGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRRRSSPHFMVEVKGDLTAKKMWLALLELAQQDHGALDCCVVVILSHGQC 240
Db 181 TGSNIDCEKLRRRSSPHFMVEVKGDLTAKKMWLALLELAQQDHGALDCCVVVILSHGQC 240
QY 241 ASHLQFPGAVYGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
Db 241 ASHLQFPGAVYGTGDCPVSVVEKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQGLRTFDQDLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQGLRTFDQDLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 10
AAB84374
ID AAB84374 standard; protein; 416 AA.
XX
AC AAB84374;
XX
DT 22-AUG-2001 (first entry)
XX
DE Amino acid sequence of aspartate-specific cysteine protease Mch6.
XX
KW Human; apoptotic protease; Mch6; aspartate-specific cysteine protease;
KW cell death; cancer; autoimmune disease; systemic lupus erythematosus;
KW viral infection; degenerative disorder; Alzheimer's disease;
KW Parkinson's disease; myelodysplastic syndrome; myocardial infarction;
KW stroke.
XX
OS Homo sapiens.
XX
PN US2001006779-Al.
XX
PD 05-JUL-2001.
XX
PF 29-MAY-1997; 97US-00865579.
XX
PR 29-MAY-1997; 97US-00865579.
XX
PA (ALNE/) ALNEMRI E S.
PA (FERN/) FERNANDES-ALNEMRI T.
PA (LITW/) LITWACK G.
XX
PI Alnemri ES, Fernandes-Alnemri T, Litwack G;
XX
DR WPI; 2001-389294/41.
XX
DR N-PSDB; AAH25191.
XX
PT Isolated gene encoding a human apoptotic protease known as Mch6, useful
PT in the diagnosis or treatment of cell death-mediated conditions, e.g.
```

PT cancers and autoimmune diseases such as systemic lupus erythematosus.

XX Claim 8; Fig 1A-C; 15pp; English.

XX The present sequence represents a human apoptotic protease, designated
CC Mch6. Mch6 is an aspartate-specific cysteine protease. Mch6 polypeptides
CC and polynucleotides can be used to diagnose, treat or reduce the severity
CC of cell death-mediated conditions, e.g. cancers, autoimmune diseases such
CC as systemic lupus erythematosus, viral infections such as herpesvirus,
CC degenerative disorders such as Alzheimer's disease and Parkinson's
CC disease, myelodysplastic syndromes such as myocardial infarction and
CC stroke. They can also be used to screen for compounds that inhibit or
CC promote Mch6 mediated apoptosis

XX Sequence 416 AA;

Query Match 98.8%; Score 2153; DB 4; Length 416;
Best Local Similarity 98.8%; Pred. No. 6.9e-217;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRRCRLRLVEQLVDQLWDVLLSRFLRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRRCRLRLVEQLVDQLWDVLLSRFLRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRIKPEV 120
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRIKPEV 120
QY 121 LRPETRPVVDIGSGGFDVGALSLRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180
Db 121 LRPETRPVVDIGSGGFDVGALSLRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRFRFSLHFWVEVKGDLTAKKMWLALLELARDHGDALDCVVVILSHGCG 240
Db 181 TGSNIDCEKLRFRFSPHFWVEVKGDLTAKKMWLALLELARDHGDALDCVVVILSHGCG 240
QY 241 ASHLQPPGAVYGTDCGCVSVEKIVNFNGTSCPSLGKPKLFFIOACGGEQKHGFEVAS 300
Db 241 ASHLQPPGAVYGTDCGCVSVEKIVNFNGTSCPSLGKPKLFFIOACGGEQKHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416

RESULT 11
ABB82738
ID ABB82738 standard; protein; 416 AA.

XX AC ABB82738;
XX 07-MAR-2003 (first entry)
XX Human caspase-9 polypeptide.
XX Caspase-9; TUCAN; cancer; biomarker; cIAP2; Apaf1; Bcl-2; Smac; human.
XX Homo sapiens.
XX WO200290931-A2.
XX 14-NOV-2002.
XX 07-MAY-2002; 2002WO-US014487.
XX 07-MAY-2001; 2001US-0289223P.
XX 12-FEB-2002; 2002US-0356934P.
XX (BURN-) BURNHAM INST.

XX Reed JC;
PT XX
DR XX
XX WPI; 2003-111999/10.

XX Determining a prognosis for survival for a cancer patient, useful for
PT determining if the patient is at risk for relapse, comprises measuring a
PT level of TUCAN in a sample from the patient, and comparing it to a
PT reference level.

XX Example; Page 125-126; 153pp; English.

XX The invention relates to determining a prognosis for survival for a
CC cancer patient. The method involves (a) measuring a level of a tumour up-
CC regulated CARD-containing antagonist of caspase-9 (TUCAN) in a neoplastic
CC cell-containing sample from the cancer patient; and (b) comparing the
CC level of TUCAN in the sample to a reference level of TUCAN, where a low
CC level of TUCAN in the sample correlates with increased survival of the
CC patient. Alternatively, the method involves measuring levels of TUCAN and
CC one or more biomarkers selected from the group of cIAP2, Apaf1, Bcl-2, or
CC Smac in a neoplastic cell-containing sample from the cancer patient. The
CC method is useful for determining if the patient is at risk for relapse,
CC or for determining a proper course of treatment for a patient with
CC cancer. The method is also useful for monitoring the effectiveness of a
CC course of treatment for a patient with cancer, e.g. colon cancer,
CC gastrointestinal cancer, breast cancer, ovarian cancer, lung cancer,
CC leukemia, CNS cancer, melanoma, prostate cancer, or renal cancer. The
CC present sequence represents a human caspase-9 polypeptide

XX Sequence 416 AA;

Query Match 98.8%; Score 2153; DB 6; Length 416;
Best Local Similarity 98.8%; Pred. No. 6.9e-217;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRRCRLRLVEQLVDQLWDVLLSRFLRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRRCRLRLVEQLVDQLWDVLLSRFLRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRIKPEV 120
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRIKPEV 120
QY 121 LRPETRPVVDIGSGGFDVGALSLRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180
Db 121 LRPETRPVVDIGSGGFDVGALSLRGNADLAYILSMPECGHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRFRFSLHFWVEVKGDLTAKKMWLALLELARDHGDALDCVVVILSHGCG 240
Db 181 TGSNIDCEKLRFRFSPHFWVEVKGDLTAKKMWLALLELARDHGDALDCVVVILSHGCG 240
QY 241 ASHLQPPGAVYGTDCGCVSVEKIVNFNGTSCPSLGKPKLFFIOACGGEQKHGFEVAS 300
Db 241 ASHLQPPGAVYGTDCGCVSVEKIVNFNGTSCPSLGKPKLFFIOACGGEQKHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416

RESULT 12
ADE52020
ID ADE52020 standard; protein; 416 AA.
XX AC ADE52020;
XX 29-JAN-2004 (first entry)
XX Human mammalian ced-3 homologue 6 (Mch6).

CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
CC identifying a compound that inhibits the peptide or polypeptide,
CC producing a compound for inhibiting or enhancing for inhibiting in a cell, and
CC a process for the manufacture of a compound for inhibiting or enhancing
CC apoptosis in a cell. The nucleic acid molecules and peptides or
CC polypeptides are useful for inducing apoptosis and identifying inhibitors
CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
CC ischaemic injury, cancer, autoimmune diseases. The present sequence
CC represents the caspase-9 protein mutated to ablate the autocatalytic
CC cleavage site in the linker region. Note: the present sequence is not
CC shown in the specification but was created by the indexer using the
CC information in the claims and the wild type caspase-9 sequence.
XX
XX
SQ Sequence 416 AA;

Query Match 98.6%; Score 2150; DB 6; Length 416;
Best Local Similarity 98.8%; Pred. No. 1.4e-216;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGLSKPTLENLTPVVLPEIRKPEV 60
DB 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRTNRQAGLSKPTLENLTPVVLPEIRKPEV 60
QY 61 DLETRGSQALPLFISCLDGTGDMLASFLRTNRQAGLSKPTLENLTPVVLPEIRKPEV 120
DB 61 DLETRGSQALPLFISCLDGTGDMLASFLRTNRQAGLSKPTLENLTPVVLPEIRKPEV 120
QY 121 LRPETRPVVDIGSGFGDVGALSLRGADLALYILSMPCGHCLINNNVFCRESGLRTR 180
DB 121 LRPETRPVVDIGSGFGDVGALSLRGADLALYILSMPCGHCLINNNVFCRESGLRTR 180
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DB 181 TGSNDCEKLRFRFSSLHPWVKGDLTAKKVLALLELARODHGDALDCCVVVILSHGQQ 240
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DB 241 ASHLQFPGAVYGTDCGVPVSEKIVNFNGTSCPSLGGKPKLFFIOACGGEQKHGFEVAS 300
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DB 301 TSPDESPGSPNPEPATPQEGRLTFDQDLAISSLTPSDIFVSVSTPFGFVSWRDPKSG 360
QY 361 SWVETLDDIFQWAHSEDLQSLILRVANAVSVKGIYKQMPGCENFLRKKLFFKTS 416
DB 361 SWVETLDDIFQWAHSEDLQSLILRVANAVSVKGIYKQMPGCENFLRKKLFFKTS 416

RESULT 14
ADA10676
ID ADA10676 standard; protein; 416 AA.
XX
AC ADA10676;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human caspase-9 protein E306A/D315A/D330A mutant.
XX
KW Human; caspase-9; anti-HIV; neurotropic; neuroprotective; vasotropic;
KW cytosolic; immunosuppressive; inhibitor of apoptosis protein; IAP;
KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
KW ischaemic injury; cancer; autoimmune disease; mutant; mutein.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 306
FT FT
FT Misc-difference 315

FT Misc-difference 330 /note= "Wild-type Asp substituted by Ala"
FT FT
XX /note= "Wild-type Asp substituted by Ala"
PN US2002160975-A1.
PD 31-OCT-2002.
XX
PF 06-FEB-2002; 2002US-00068569.
XX
PR 08-FEB-2001; 2001US-0267966P.
PR 24-AUG-2001; 2001US-00939293.
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 2003-219992/21.
XX
PT New nucleic acid molecules encoding a peptide or polypeptide that binds
PT to a portion of an inhibitor of apoptosis protein, useful for inducing
PT apoptosis and identifying inhibitors or enhancers of apoptosis for
PT treating AIDS, or cancer.
XX
PS Claim 38; Page; 52pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule comprising a
XX polynucleotide that encodes a polypeptide or peptide, or its variants
XX that specifically binds to at least a portion of an inhibitor of
XX apoptosis protein (IAP). Also included are a peptide or a polypeptide
XX (comprising at least an N terminus sequence of caspase-9 N-terminal
XX linker sequence, a first portion of a procaspase-9 that specifically
XX binds at least a portion of an IAP and a second portion of a procaspase-9
XX containing a mutated active site, where the peptide or polypeptide
XX specifically binds at least a portion of an IAP and lacks cysteine
XX protease activity, and at least a portion of caspase-3, where the peptide
XX or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
XX an IAP or an IAP Bir3 domain) or at least a portion of a mutated
XX procaspase-9, which fails to undergo normal processing and possesses wild
XX type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
XX polynucleotide sequence that encodes the caspase-9 N-terminal linker, an
XX expression vector comprising any of the nucleic acids, a host cell
XX containing the expression vector, an antibody that specifically binds to
XX the peptide or polypeptide, an antibody that specifically binds to an
XX epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
XX in a cell or stimulating apoptosis in a neoplastic or tumour cell,
XX identifying an inhibitor or enhancer of caspase-mediated apoptosis,
XX identifying a compound that inhibits the peptide or polypeptide,
XX producing a compound for inhibiting or enhancing apoptosis in a cell, and
XX a process for the manufacture of a compound for inhibiting or enhancing
XX apoptosis in a cell. The nucleic acid molecules and peptides or
XX polypeptides are useful for inducing apoptosis and identifying inhibitors
XX or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
XX ischaemic injury, cancer, autoimmune diseases. The present sequence
XX represents the caspase-9 protein mutated to ablate the autocatalytic
XX cleavage site in the linker region. Note: the present sequence is not
XX shown in the specification but was created by the indexer using the
XX information in the claims and the wild type caspase-9 sequence.
XX
SQ Sequence 416 AA;

Query Match 98.3%; Score 2144; DB 6; Length 416;
Best Local Similarity 98.6%; Pred. No. 6.1e-216;
Matches 410; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
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 AC ADA10677;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human caspase-9 protein del316-330 mutant.
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 KW Human; caspase-9; anti-HIV; neurotropic; neuroprotective; vasotropic;
 KW cystostatic; immunosuppressive; inhibitor of apoptosis protein; IAP;
 KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
 KW Bcl3 domain; apoptosis; AIDS; neurodegenerative disease;
 KW ischaemic injury; cancer; autoimmune disease; mutant; mutuin.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 315..316
 FT /note= "Residues 316-330 of the wild-type protein have
 been deleted"
 XX
 FN US2002160975-A1.
 XX
 PD 31-OCT-2002.
 XX
 PF 06-FEB-2002; 2002US-00068569.
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 PR 08-FEB-2001; 2001US-0267966P.
 PR 24-AUG-2001; 2001US-00939293.
 XX
 PA (UWJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Alnemri ES;
 XX
 DR WPI; 2003-219992/21.
 XX
 PT New nucleic acid molecules encoding a peptide or polypeptide that binds
 PT to a portion of an inhibitor of apoptosis protein, useful for inducing
 PT apoptosis and identifying inhibitors or enhancers of apoptosis for
 PT treating AIDS, or cancer.
 XX
 PS Claim 39; Page; 52pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule comprising a
 CC polynucleotide that encodes a polypeptide or peptide, or its variants
 CC that specifically binds to at least a portion of an inhibitor of
 CC apoptosis protein (IAP). Also included are a peptide or a polypeptide
 CC (comprising at least an N terminus sequence of caspase-9 N-terminal
 CC linker sequence, a first portion of a procaspase-9 that specifically

CC binds at least a portion of an IAP and a second portion of a procaspase-9
 CC containing a mutated active site, where the peptide or polypeptide
 CC specifically binds at least a portion of an IAP and lacks cysteine
 CC protease activity, and at least a portion of caspase-3, where the peptide
 CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
 CC an IAP or an IAP Bcl3 domain) or at least a portion of a mutated
 CC procaspase-9, which fails to undergo normal processing and possesses wild
 CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
 CC polynucleotide sequence that encodes the caspase-9 N-terminal linker), an
 CC expression vector comprising any of the nucleic acids, a host cell
 CC containing the expression vector, an antibody that specifically binds to
 CC the peptide or polypeptide, an antibody that specifically binds to an
 CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
 CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
 CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
 CC identifying a compound that inhibits the peptide or polypeptide,
 CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
 CC a process for the manufacture of a compound for inhibiting or enhancing
 CC apoptosis in a cell. The nucleic acid molecules and peptides or
 CC polypeptides are useful for inducing apoptosis and identifying inhibitors
 CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
 CC ischaemic injury, cancer, autoimmune diseases. The present sequence
 CC represents the caspase-9 protein mutated to ablate the autocatalytic
 CC cleavage site in the linker region. Note: the present sequence is not
 CC shown in the specification but was created by the indexer using the
 CC information in the claims and the wild type caspase-9 sequence.
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Query March 94.9%; Score 2069.5; DB 6; Length 401;
 Best Local Similarity 95.7%; Pred. No. 3.9e-208;
 Matches 398; Conservative 1; Mismatches 2; Indels 15; Gaps 1;

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 Db |||||||
 QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLLFFKTS 416
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 Job time : 55 secs

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OM protein - protein search, using sw model

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2166	99.4	416	13	US-10-068-569-1
2	2157	98.9	416	9	US-09-954-697-30
3	2153	98.8	416	10	US-09-851-873-102
4	2153	98.8	416	12	US-09-746-731-2
5	2153	98.8	416	13	US-10-059-749-2
6	2153	98.8	416	14	US-10-141-618-4
7	1282	58.8	266	15	US-10-116-275-172
8	773	35.5	159	12	US-10-424-599-174531
9	468	21.5	93	13	US-10-014-269-27
10	468	21.5	93	13	US-10-002-974-27
11	468	21.5	93	14	US-10-314-506-27
12	419	19.2	277	15	US-10-155-567-4
13	418	19.2	264	13	US-10-103-448-3
14	418	19.2	264	13	US-10-108-929-3
15	418	19.2	277	9	US-09-895-263-4

16	418	19.2	277	9	US-09-954-697-12	Sequence 12, Appl
17	418	19.2	277	10	US-09-851-873-98	Sequence 98, Appl
18	418	19.2	277	12	US-10-232-884-4	Sequence 4, Appl
19	418	19.2	277	14	US-10-214-932-108	Sequence 108, App
20	418	19.2	277	14	US-10-207-655-202	Sequence 202, App
21	418	19.2	277	14	US-10-280-670-5	Sequence 5, Appl
22	418	19.2	277	15	US-10-368-438-30	Sequence 30, Appl
23	418	19.2	277	16	US-10-408-765A-172	Sequence 172, App
24	418	19.2	277	16	US-10-701-490-11	Sequence 11, Appl
25	409.5	18.8	284	12	US-10-232-884-5	Sequence 5, Appl
26	378	17.3	286	9	US-09-862-915-1	Sequence 1, Appl
27	371.5	17.0	335	15	US-10-368-438-16	Sequence 16, Appl
28	361.5	16.6	303	9	US-09-944-851-2	Sequence 2, Appl
29	361.5	16.6	303	9	US-09-954-697-24	Sequence 24, Appl
30	361.5	16.6	303	10	US-09-851-873-100	Sequence 100, App
31	361.5	16.6	303	14	US-10-337-060-2	Sequence 2, Appl
32	361.5	16.6	303	14	US-10-280-670-4	Sequence 4, Appl
33	354.5	16.3	303	9	US-09-895-263-2	Sequence 2, Appl
34	344.5	15.8	389	14	US-10-280-670-2	Sequence 2, Appl
35	341.5	15.7	389	14	US-10-280-670-3	Sequence 3, Appl
36	311.5	14.3	293	9	US-09-954-697-21	Sequence 21, Appl
37	311.5	14.3	354	9	US-09-888-243-20	Sequence 20, Appl
38	304	13.9	312	8	US-08-459-455-53	Sequence 53, Appl
39	303.5	13.9	266	15	US-10-368-438-20	Sequence 20, Appl
40	303.5	13.9	293	10	US-09-851-873-99	Sequence 99, Appl
41	303.5	13.9	293	14	US-10-171-077-5	Sequence 5, Appl
42	303.5	13.9	293	14	US-10-280-670-6	Sequence 6, Appl
43	303.5	13.9	293	15	US-10-368-438-31	Sequence 31, Appl
44	294	13.5	147	14	US-10-214-932-110	Sequence 110, App
45	294	13.5	285	9	US-09-954-697-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1

US-10-068-569-1
; Sequence 1, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; FILE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-1

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Matches 413; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db	61	DLETRGSQALFLFISCTEDTQDMLASFLRNROAKLSKPTLENLTVPVLRPEIRKPEV	120
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Db	121	LRPETRPVDIGSGFGDVGALSLRGNADLAYILSMPCGCHLIINNVCRESGLRTR	180
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RESULT 2
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; Sequence 30, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE OF INVENTION: THERIOF
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-30
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; Sequence 102, Application US/09851873
; Publication No. US20030165488A1
; GENERAL INFORMATION:
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; APPLICANT: Kletzien, Rolf P
; APPLICANT: Readon, Ilene M
; APPLICANT: Weiland, Katherine L
; TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
; FILE REFERENCE: 28341/00233
; CURRENT APPLICATION NUMBER: US/09/851,873
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 102
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
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Db 121 LRPETPRPVDIGSGGFDVGALSLRGADLAVILSMPCGHCLIIINNPNFCRESGLRTR 180
QY 181 TGSNDCEKLRRLRRFSSLHFMVEVKGDLTAKKMWLALLELAQDHGALDCVVVILSHGCG 240
Db 181 TGSNDCEKLRRLRRFSSLHFMVEVKGDLTAKKMWLALLELAQDHGALDCVVVILSHGCG 240
QY 241 ASHLQPPGAVYGTGDCPVSVKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
Db 241 ASHLQPPGAVYGTGDCPVSVKIVNIFNGTSCPSLGGKPKLFFIOACGGEQKDHGFEVAS 300
QY 301 TSPDESPOGSPNEPDATPFQEGRLTFDQDLAISSLPDIFVSYSTFFGFSWRDPKSG 360
Db 301 TSPDESPOGSPNEPDATPFQEGRLTFDQDLAISSLPDIFVSYSTFFGFSWRDPKSG 360
QY 361 SWVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKOMPCCFNFLRKKLFFKTS 416
Db 361 SWVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKOMPCCFNFLRKKLFFKTS 416
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RESULT 4
US-09-746-731-2
; Sequence 2, Application US/09746731
; Publication No. US20010016345A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/746,731
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; FILING DATE: 22-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-746-731-2

Query Match          98.8%; Score 2153; DB 12; Length 416;
Best Local Similarity 98.8%; Pred. No. 2.3e-205;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGSRDDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGSRDDQARQLII 60
Qy 61 DLETRGSQLPLFTSCLEDTGQDMLASFLRNRQAGLSKPTLENLTPVVLRLPEIRKEV 120
Db 61 DLETRGSQLPLFTSCLEDTGQDMLASFLRNRQAGLSKPTLENLTPVVLRLPEIRKEV 120
Qy 121 LRPTPRPVDIGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
Db 121 LRPTPRPVDIGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
Qy 181 TGSNIDCEKLRRRSSLHFVVEVKGDLTAKQWVLLALLELARQDHGALDCCVVVILSHGCQ 240
Db 181 TGSNIDCEKLRRRSSLHFVVEVKGDLTAKQWVLLALLELARQDHGALDCCVVVILSHGCQ 240
Qy 241 ASHLQFFGAVYGTGCPVSVKEKVIINFGTSCPSLGGKPKLFFIQACGGEQKHGFVEAS 300
Db 241 ASHLQFFGAVYGTGCPVSVKEKVIINFGTSCPSLGGKPKLFFIQACGGEQKHGFVEAS 300
Qy 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPFGVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPFGVSWRDPKSG 360
Qy 361 SWVYETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCNFKLFFKTS 416
Db 361 SWVYETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCNFKLFFKTS 416

RESULT 5
US-10-059-749-2
; Sequence 2, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Enad S.
;               Fernandes-Alnemri, Teresa
;               Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
;               Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-059-749-2

Query Match          98.8%; Score 2153; DB 13; Length 416;
Best Local Similarity 98.8%; Pred. No. 2.3e-205;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGSRDDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGSRDDQARQLII 60
Qy 61 DLETRGSQLPLFTSCLEDTGQDMLASFLRNRQAGLSKPTLENLTPVVLRLPEIRKEV 120
Db 61 DLETRGSQLPLFTSCLEDTGQDMLASFLRNRQAGLSKPTLENLTPVVLRLPEIRKEV 120
Qy 121 LRPTPRPVDIGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
Db 121 LRPTPRPVDIGSGFGDVGALSLRGNADLAYILSMPECGHCLIIINNVPFCRESGLRTR 180
Qy 181 TGSNIDCEKLRRRSSLHFVVEVKGDLTAKQWVLLALLELARQDHGALDCCVVVILSHGCQ 240
Db 181 TGSNIDCEKLRRRSSLHFVVEVKGDLTAKQWVLLALLELARQDHGALDCCVVVILSHGCQ 240
Qy 241 ASHLQFFGAVYGTGCPVSVKEKVIINFGTSCPSLGGKPKLFFIQACGGEQKHGFVEAS 300
Db 241 ASHLQFFGAVYGTGCPVSVKEKVIINFGTSCPSLGGKPKLFFIQACGGEQKHGFVEAS 300
Qy 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPFGVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPFGVSWRDPKSG 360
Qy 361 SWVYETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCNFKLFFKTS 416
Db 361 SWVYETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCNFKLFFKTS 416

RESULT 6
US-10-141-618-4
; Sequence 4, Application US/10141618
; Publication No. US20030165887A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods For Determining the Prognosis
; TITLE OF INVENTION: For Cancer Patients Using Tucan
; FILE REFERENCE: P-LJ 5254
; CURRENT APPLICATION NUMBER: US/10/141,618
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,233
; PRIOR FILING DATE: 2001-05-07

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; PRIOR APPLICATION NUMBER: US 60/356,934
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US 09/388,221
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-141-618-4

Query Match          98.8%; Score 2153; DB 14; Length 416;
Best Local Similarity 98.8%; Pred. No. 2.3e-205;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSELFRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSELFRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTRNQAGLSKPTLENLTPVWLRPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTRNQAGLSKPTLENLTPVWLRPEIRKPEV 120
QY 121 LRPETPRPVDIGSGGFGDVGALESURGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
Db 121 LRPETPRPVDIGSGGFGDVGALESURGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
QY 121 LRPETPRPVDIGSGGFGDVGALESURGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
Db 121 LRPETPRPVDIGSGGFGDVGALESURGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRFFSLHFMVEVKGLTAKKMWLALLELARQDHGALDCCVVVILSHGQ 240
Db 181 TGSNIDCEKLRRLRFFSLHFMVEVKGLTAKKMWLALLELARQDHGALDCCVVVILSHGQ 240
QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTRNQAGLSKPTLENLTPVWLRPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTRNQAGLSKPTLENLTPVWLRPEIRKPEV 120
QY 121 LRPETPRPVDIGSGGFGDVGALESURGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
Db 121 LRPETPRPVDIGSGGFGDVGALESURGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRFFSLHFMVEVKGLTAKKMWLALLELARQDHGALDCCVVVILSHGQ 240
Db 181 TGSNIDCEKLRRLRFFSLHFMVEVKGLTAKKMWLALLELARQDHGALDCCVVVILSHGQ 240
QY 241 ASHLQPGAVGYTDCGVPVSVEKIVNFNGTSCPSLGKPKLFFIOACGGEQKDHGFEVAS 300
Db 241 ASHLQPGAVGYTDCGVPVSVEKIVNFNGTSCPSLGKPKLFFIOACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 7
US-10-116-275-172
; Sequence 172, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20087
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-172

Query Match          58.8%; Score 1282; DB 15; Length 266;
Best Local Similarity 63.2%; Pred. No. 7.1e-119;
Matches 263; Conservative 0; Mismatches 3; Indels 150; Gaps 1;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSELFRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSELFRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTRNQAGLSKPTLENLTPVWLRPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTRNQAGLSKPTLENLTPVWLRPEIRKPEV 120
QY 121 LRPETPRPVDIGSGGFGDVGALESURGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
Db 121 LRPETPRPVDIGSGGFGDVGALESURGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
QY 121 LRPETPRPVDIGSGGFGDVGALESURGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
Db 121 LRPETPRPVDIGSGGFGDVGALESURGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRFFSLHFMVEVKGLTAKKMWLALLELARQDHGALDCCVVVILSHGQ 240
Db 181 TGSNIDCEKLRRLRFFSLHFMVEVKGLTAKKMWLALLELARQDHGALDCCVVVILSHGQ 240
QY 241 ASHLQPGAVGYTDCGVPVSVEKIVNFNGTSCPSLGKPKLFFIOACGGEQKDHGFEVAS 300
Db 241 ASHLQPGAVGYTDCGVPVSVEKIVNFNGTSCPSLGKPKLFFIOACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 9
US-10-014-269-27
; Sequence 27, Application US/10014269
; Publication No. US20020127673A1
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QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSELFRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSELFRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTRNQAGLSKPTLENLTPVWLRPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTRNQAGLSKPTLENLTPVWLRPEIRKPEV 120
QY 121 LRPETPRPVDIGSGGFGDVGALESURGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
Db 121 LRPETPRPVDIGSGGFGDVGALESURGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRFFSLHFMVEVKGLTAKKMWLALLELARQDHGALDCCVVVILSHGQ 240
Db 181 TGSNIDCEKLRRLRFFSLHFMVEVKGLTAKKMWLALLELARQDHGALDCCVVVILSHGQ 240
QY 241 ASHLQPGAVGYTDCGVPVSVEKIVNFNGTSCPSLGKPKLFFIOACGGEQKDHGFEVAS 300
Db 241 ASHLQPGAVGYTDCGVPVSVEKIVNFNGTSCPSLGKPKLFFIOACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPDESFGSNPEPDATPFQEGRLTFDQDLDAISSLPTSDIFVSYSTPFGFVSWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
Db 361 SWYVETLDDIFEQWAHSEDLSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416

RESULT 8
US-10-424-599-174531
; Sequence 174531, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 174531
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_12861C.1.pcp
US-10-424-599-174531

Query Match          35.5%; Score 773; DB 12; Length 159;
Best Local Similarity 96.9%; Pred. No. 1.7e-68;
Matches 154; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSELFRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSELFRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTRNQAGLSKPTLENLTPVWLRPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLEDTGQDMLASFLRTRNQAGLSKPTLENLTPVWLRPEIRKPEV 120
QY 121 LRPETPRPVDIGSGGFGDVGALESURGNADLAYILSMPE 159
Db 121 LRPETPRPVDIGSGGFGDVGALESURGNADLAYILSMPE 159

RESULT 9
US-10-014-269-27
; Sequence 27, Application US/10014269
; Publication No. US20020127673A1
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```
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogura, Yasunori
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06645
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-269-27

Query Match      21.5%; Score 468; DB 13; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.9e-38;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

QY 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNR 93
Db 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNR 93

RESULT 10
US-10-002-974-27
; Sequence 27, Application US/10002974
; Publication No. US20020197616A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogura, Yasunori
; APPLICANT: Cho, Judy
; APPLICANT: Nicolae, Dan I.
; APPLICANT: Bonen, Denise
; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
; FILE REFERENCE: UM-06646
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-974-27

Query Match      21.5%; Score 468; DB 13; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.9e-38;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

QY 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNR 93
Db 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNR 93

RESULT 11
US-10-314-506-27
; Sequence 27, Application US/10314506
; Publication No. US20030175762A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Ogura, Yasunori
```

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; TITLE OF INVENTION: Modulators of NOD2 Signaling
; FILE REFERENCE: UM-06984
; CURRENT APPLICATION NUMBER: US/10/314,506
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 10,014,269
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/244,289
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-314-506-27

Query Match      21.5%; Score 468; DB 14; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.9e-38;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60

QY 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNR 93
Db 61 DLETRGSQLPLFISCLDGTQDMLASFLRTNR 93

RESULT 12
US-10-155-567-4
; Sequence 4, Application US/10155567
; Publication No. US20030219421A1
; GENERAL INFORMATION:
; APPLICANT: CHRISTAKOS, Sylvia
; TITLE OF INVENTION: CALBINDIN-D 28K PROTECTION AGAINST GLUCOCORTICOID INDUCED CELL DEATH
; FILE REFERENCE: 267/266
; CURRENT APPLICATION NUMBER: US/10/155,567
; CURRENT FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 277
; TYPE: PRT
; ORGANISM: homosapiens
US-10-155-567-4

Query Match      19.2%; Score 419; DB 15; Length 277;
Best Local Similarity 33.2%; Pred. No. 7.4e-33;
Matches 91; Conservative 50; Mismatches 91; Indels 42; Gaps 4;

QY 150 DLAYILSMFPCGHCLIIINNVNFCRESGLRTRTSGNIDCEKLRRFFSLHFVVEVKGDLTA 209
Db 34 DTGKMDYPEWGLCIILNNKNFKHSTGWTSGTDDVDAAANLRETFRLNKYEVRNKNDLTR 93

QY 210 KKMVLALELARQDHGALDCCVVVILSHGQASHLOFPFGAVYGTGDCPVSVEKIVNIFNG 269
Db 94 EEIVELMRDVSKEHDSKRSSFVVCVLLSHGEE-----GIIFGTNG-PVDLKKITNFRG 145

QY 270 TSPESLGGKPKLFFIQACGGEQKHGFEVASTSPEDSPGSPNPEPDATPFQEGRLTDFQL 329
Db 146 DRCRLTGKPKLFIQACRGTELDGCIETDGSVDDDM----- 182

QY 330 DAISSLPTSPDIFVSYSTPFGVSWRDPKSGSVVETLDDIFQWAHSEDLQSILLRVAN 389
Db 183 -ACHKIPVDADFLYAYSTAPGYTSWRNSKDGSWFIOSLCAMLKQYADKLEFMHILTRVNR 241

QY 390 AVSVK-----GIYKQMPGCFNPLRKKLFF 413
Db 242 KVATEFESFSFDATEFHAKKQIPCVISMLTKELYF 275

RESULT 13
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US-10-103-448-3
; Sequence 3, Application US/10103448
; Publication No. US20020155579A1
; GENERAL INFORMATION:
; APPLICANT: Krebs, Joseph F.
; APPLICANT: Srinivasan, Anu
; APPLICANT: Fritz, Lawrence C.
; APPLICANT: Wu, Joseph C.
; TITLE OF INVENTION: MEMBRANE DERIVED CASPASE-3, COMPOSITIONS
; TITLE OF INVENTION: COMPRISING THE SAME AND METHODS OF USE THEREFOR
; FILE REFERENCE: 480140.468D1
; CURRENT APPLICATION NUMBER: US/10/103,448
; CURRENT FILING DATE: 2002-03-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-103-448-3

Query Match          19.2%; Score 418; DB 13; Length 264;
Best Local Similarity 33.2%; Pred. No. 8.6e-33;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAYILSMPECGHCLIIINNVCRESGLRTRTGSNIDCEKLRFRSSLHFMVEVKGDLTA 209
DB 21 DNSYKMDYPEMGLCIIINNKNFKHSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTR 80

QY 210 KKMVLALLELARQDHGALDCCVVWILSHGCOASHLQFPQAVYGTGDCPVSVKEIWNIFNG 269
DB 81 EEIVELMRDVSKEHSHKRSFVCLLSHGEE-----GIIFGTNG-PVDLKKITNFFRG 132

QY 270 TSCPSLGGKPKLFFIQACGGQKHGFEVASTSPEDSPGSPNPDATPFQEGLRFTDOL 329
DB 133 DCRSLTGKPKLFIQACRGTELDGCIETDGSVDDM----- 169

QY 330 DAISLPTSDIFVSYSTPFGVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVAN 389
DB 170 -ACHKIPVDADFLYAYSTAGYYSWRNSKDSWFIQSLCAMLKQYADKLEFPHMLTRVNR 228

QY 390 AVSVK-----GIYKQMPGCFNFKKLPFF 413
DB 229 KVATEFESFSDATPHAKKQIPCIIVSMLTKELYF 262

RESULT 14
US-10-108-929-3
; Sequence 3, Application US/10108929
; Publication No. US20020197702A1
; GENERAL INFORMATION:
; APPLICANT: Krebs, Joseph F.
; APPLICANT: Srinivasan, Anu
; APPLICANT: Fritz, Lawrence C.
; APPLICANT: Wu, Joseph C.
; TITLE OF INVENTION: MEMBRANE DERIVED CASPASE-3, COMPOSITIONS
; TITLE OF INVENTION: COMPRISING THE SAME AND METHODS OF USE THEREFOR
; FILE REFERENCE: 480140.468D2
; CURRENT APPLICATION NUMBER: US/10/108,929
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-108-929-3

Query Match          19.2%; Score 418; DB 13; Length 264;
Best Local Similarity 33.2%; Pred. No. 8.6e-33;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAYILSMPECGHCLIIINNVCRESGLRTRTGSNIDCEKLRFRSSLHFMVEVKGDLTA 209
DB 21 DNSYKMDYPEMGLCIIINNKNFKHSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTR 80

QY 210 KKMVLALLELARQDHGALDCCVVWILSHGCOASHLQFPQAVYGTGDCPVSVKEIWNIFNG 269
DB 81 EEIVELMRDVSKEHSHKRSFVCLLSHGEE-----GIIFGTNG-PVDLKKITNFFRG 132

QY 270 TSCPSLGGKPKLFFIQACGGQKHGFEVASTSPEDSPGSPNPDATPFQEGLRFTDOL 329
DB 133 DCRSLTGKPKLFIQACRGTELDGCIETDGSVDDM----- 169

QY 330 DAISLPTSDIFVSYSTPFGVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVAN 389
DB 170 -ACHKIPVDADFLYAYSTAGYYSWRNSKDSWFIQSLCAMLKQYADKLEFPHMLTRVNR 228

QY 390 AVSVK-----GIYKQMPGCFNFKKLPFF 413
DB 229 KVATEFESFSDATPHAKKQIPCIIVSMLTKELYF 262
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DB 21 DNSYKMDYPEMGLCIIINNKNFKHSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTR 80
QY 210 KKMVLALLELARQDHGALDCCVVWILSHGCOASHLQFPQAVYGTGDCPVSVKEIWNIFNG 269
DB 81 EEIVELMRDVSKEHSHKRSFVCLLSHGEE-----GIIFGTNG-PVDLKKITNFFRG 132
QY 270 TSCPSLGGKPKLFFIQACGGQKHGFEVASTSPEDSPGSPNPDATPFQEGLRFTDOL 329
DB 133 DCRSLTGKPKLFIQACRGTELDGCIETDGSVDDM----- 169
QY 330 DAISLPTSDIFVSYSTPFGVSWRDPKSGSWYVETLDDIFEQWAHSEDLSLLLRVAN 389
DB 170 -ACHKIPVDADFLYAYSTAGYYSWRNSKDSWFIQSLCAMLKQYADKLEFPHMLTRVNR 228
QY 390 AVSVK-----GIYKQMPGCFNFKKLPFF 413
DB 229 KVATEFESFSDATPHAKKQIPCIIVSMLTKELYF 262

RESULT 15
US-09-895-263-4
; Sequence 4, Application US/09895263
; Patent No. US20020076793A1
; GENERAL INFORMATION:
; APPLICANT: He, Wei-Wu et al.
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
; LIKE Apoptosis Protease 3 and 4
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/895,263
; FILING DATE: 02-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jonathan L. Klein
; REGISTRATION NUMBER: 41,119
; REFERENCE/DOCKET NUMBER: PF140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-251-6015
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-895-263-4

Query Match          19.2%; Score 418; DB 9; Length 277;
Best Local Similarity 33.2%; Pred. No. 9.3e-33;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAYILSMPECGHCLIIINNVCRESGLRTRTGSNIDCEKLRFRSSLHFMVEVKGDLTA 209
DB 34 DNSYKMDYPEMGLCIIINNKNFKHSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTR 93
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Qy	210	KKWVLALELAROQDHGALDCCVVVILSHGCOASHLQFFGAVYGTDCFPVSVEKIVNIENG	269
Db	94	BEIVELMDVSKEDHSKRSSFVCLLSHGE-----GIIFGTNG-EVDLKKITNFFRG	145
Qy	270	TSCPGLGKPKLFFFIQACGGEQKHGFEVASTSPEDSPGSGNPEDATPFOEGLRTFDQL	329
Db	146	DRCSLTGKPKLFIQACGTELDGCIETDSGVDDM-----	182
Qy	330	DAISLPTPSDIFVSYSTFGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLILRVAN	389
Db	183	-ACHKIPVEADFLYAYSTAPGYISWRNSKDGSWFIQSLCAMLKQVADKLEFMHILTRVN	241
Qy	390	AVSVK-----GIYKQMPGCENFLRKLFF	413
Db	242	KVATEFESFPDATFHAKKQIPCIVSMULTKELYF	275

Search completed: August 3, 2004, 09:08:22
Job time : 46 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 09:00:26 ; Search time 19 Seconds
(without alignments)

1130.337 Million cell updates/sec

Title: US-09-961-201A-1

Perfect score: 2180

Sequence: 1 MDEADRLRLRRLRVLEL.....YKQMPGCFNLRKLFFKTS 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 352840

Minimum DB seq length: 0

Maximum DB seq length: 416

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2180	100.0	416	3	US-08-852-936C-1
2	2180	100.0	416	3	US-09-300-328-1
3	2180	100.0	416	4	US-09-069-023-23
4	2157	98.9	416	4	US-09-561-756-30
5	2157	98.9	416	4	US-09-227-721-30
6	2157	98.9	416	4	US-09-954-697-30
7	2153	98.8	416	3	US-09-257-218-2
8	2153	98.8	416	3	US-09-311-760-2
9	2153	98.8	416	4	US-08-863-579-2
10	2153	98.8	416	4	US-10-059-749-2
11	1083	49.7	203	3	US-08-852-936C-4
12	1083	49.7	203	3	US-09-300-328-4
13	418	19.2	277	3	US-08-591-605-2
14	418	19.2	277	3	US-08-964-308-6
15	418	19.2	277	3	US-08-462-969B-4
16	418	19.2	277	3	US-08-964-313-6
17	418	19.2	277	4	US-09-069-138-6
18	418	19.2	277	4	US-09-561-756-12
19	418	19.2	277	4	US-09-227-721-12
20	418	19.2	277	4	US-08-983-502-30
21	418	19.2	277	4	US-09-124-934A-4
22	418	19.2	277	4	US-08-724-378D-5
23	418	19.2	277	4	US-08-334-251D-4
24	418	19.2	277	4	US-09-516-747-30
25	418	19.2	277	4	US-09-954-697-12
26	418	19.2	277	5	PCT-US96-10521-30
27	417	19.1	277	4	US-09-291-289-11

28 409 18.8 277 2 US-08-890-542A-2
29 408 18.7 277 3 US-08-964-308-10
30 408 18.7 277 3 US-08-964-313-10
31 408 18.7 277 4 US-09-069-138-10
32 382 17.5 389 2 US-08-618-408B-4
33 378 17.3 286 4 US-08-360-017-1
34 371.5 17.0 335 4 US-08-983-502-16
35 371.5 17.0 335 4 US-09-516-747-16
36 371.5 17.0 335 5 PCT-US96-10521-16
37 361.5 16.6 303 4 US-09-561-756-24
38 361.5 16.6 303 4 US-09-227-721-24
39 361.5 16.6 303 4 US-08-556-627A-2
40 361.5 16.6 303 4 US-08-724-378D-4
41 361.5 16.6 303 4 US-09-954-697-24
42 361.5 16.6 303 4 US-08-163-099-2
43 354.5 16.3 303 3 US-08-462-969B-2
44 354.5 16.3 303 4 US-09-124-934A-2
45 354.5 16.3 303 4 US-08-334-251D-2

ALIGNMENTS

RESULT 1
US-08-852-936C-1
; Sequence 1, Application US/08852936C
; Patent No. 6010878
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.
; APPLICANT: RUBEN, STEVEN M.
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
; TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEO for Windows Version 2.0
; CURRENT APPLICATION DATA: US/08/852,936C
; APPLICATION NUMBER: US/08/852,936C
; FILING DATE: 08-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/018,961
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: 60/020,344
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: 60/017,949
; FILING DATE: 20-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: p50483-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Sequence 2, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 4, Appli
Sequence 1, Appli
Sequence 16, Appl
Sequence 16, Appl
Sequence 24, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli

US-08-852-936C-1

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Query Match      100.0%; Score 2180; DB 3; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.3e-230;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDEADRLRLRRCLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGSRDQARQLII 60

QY 61 DLETGSQLPLFISCLDTGQDMLASFLRTRNQAGKLSKPTLENITPVVLRPEIRKPEV 120
Db 61 DLETGSQLPLFISCLDTGQDMLASFLRTRNQAGKLSKPTLENITPVVLRPEIRKPEV 120

QY 121 IRPETPRPVYDGGGFGDVGALESRLGNADLAYILSMFPCGHCLIIINNVPFCRESGLRTR 180
Db 121 IRPETPRPVYDGGGFGDVGALESRLGNADLAYILSMFPCGHCLIIINNVPFCRESGLRTR 180

QY 181 TGSNDICEKLRFRFSLHFMVEVKGDLTAKMVLALLELARODHGALDCCVVVILSHGCO 240
Db 181 TGSNDICEKLRFRFSLHFMVEVKGDLTAKMVLALLELARODHGALDCCVVVILSHGCO 240

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Db 241 ASHLQPPGAVYGTDCGCVSVEKIVNFNGTSCPSLGGKPKLFFIQACGGEQKHGFVEAS 300

QY 301 TSPEDSPGSNPEPDATPFQEGRLTFDQDLAISLPTPSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPEDSPGSNPEPDATPFQEGRLTFDQDLAISLPTPSDIFVSYSTPFGFVSWRDPKSG 360

QY 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
Db 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
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RESULT 2

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US-09-300-328-1
; Sequence 1, Application US/09300328
; Patent No. 6294169
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.
; APPLICANT: RUBEN, STEVEN M.
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
; TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/300,328
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,936
; FILING DATE: 08-MAY-1997
; APPLICATION NUMBER: 60/018,961
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: 60/020,344
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: 60/017,949
; FILING DATE: 20-MAY-1996
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: p50483-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-300-328-1

Query Match      100.0%; Score 2180; DB 3; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.3e-230;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRRCLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRLRRCLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGSRDQARQLII 60

QY 61 DLETGSQLPLFISCLDTGQDMLASFLRTRNQAGKLSKPTLENITPVVLRPEIRKPEV 120
Db 61 DLETGSQLPLFISCLDTGQDMLASFLRTRNQAGKLSKPTLENITPVVLRPEIRKPEV 120

QY 121 IRPETPRPVYDGGGFGDVGALESRLGNADLAYILSMFPCGHCLIIINNVPFCRESGLRTR 180
Db 121 IRPETPRPVYDGGGFGDVGALESRLGNADLAYILSMFPCGHCLIIINNVPFCRESGLRTR 180

QY 181 TGSNDICEKLRFRFSLHFMVEVKGDLTAKMVLALLELARODHGALDCCVVVILSHGCO 240
Db 181 TGSNDICEKLRFRFSLHFMVEVKGDLTAKMVLALLELARODHGALDCCVVVILSHGCO 240

QY 241 ASHLQPPGAVYGTDCGCVSVEKIVNFNGTSCPSLGGKPKLFFIQACGGEQKHGFVEAS 300
Db 241 ASHLQPPGAVYGTDCGCVSVEKIVNFNGTSCPSLGGKPKLFFIQACGGEQKHGFVEAS 300

QY 301 TSPEDSPGSNPEPDATPFQEGRLTFDQDLAISLPTPSDIFVSYSTPFGFVSWRDPKSG 360
Db 301 TSPEDSPGSNPEPDATPFQEGRLTFDQDLAISLPTPSDIFVSYSTPFGFVSWRDPKSG 360

QY 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
Db 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKKLFFKTS 416
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RESULT 3

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US-09-069-023-23
; Sequence 23, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Nachiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-069-023-23

Query Match      100.0%; Score 2180; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.3e-230;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 60
QY 61 DLETRGSQLPLFTISCLDTCQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 120
DB 61 DLETRGSQLPLFTISCLDTCQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 120
QY 121 LRPETPRVDIGSGGFGDVGDALESIRGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
DB 121 LRPETPRVDIGSGGFGDVGDALESIRGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRSSSHFVMEVKGDLTAKKWLALLELARQDHGALDCCVVWILSHGCQ 240
DB 181 TGSNIDCEKLRRLRRSSSHFVMEVKGDLTAKKWLALLELARQDHGALDCCVVWILSHGCQ 240
QY 241 ASHLQFPAGVGTGDCPVSVSEKI VNIENGTS CP SLGGKPKLFFFIQACGGEQKDHGFEVAS 300
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DB 301 TSPDESFGSNPEPDATPFQEGRLTFDQDAILSLPTPSDIFVSYSTFPFVSVWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKKLLFFKTS 416
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RESULT 4

US-09-561-756-30

; Sequence 30, Application US/09561756

; Patent No. 6376226

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 480140.431

; CURRENT APPLICATION NUMBER: US/09/561,756

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 09/227,721

; PRIOR FILING DATE: 1999-01-08

; NUMBER OF SEQ ID NOS: 116

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 30

; LENGTH: 416

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-561-756-30

Query Match 98.9%; Score 2157; DB 4; Length 416;
Best Local Similarity 99.0%; Pred. No. 1.7e-227;
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 60
DB 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 60
QY 61 DLETRGSQLPLFTISCLDTCQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 120
DB 61 DLETRGSQLPLFTISCLDTCQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 120
QY 121 LRPETPRVDIGSGGFGDVGDALESIRGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
DB 121 LRPETPRVDIGSGGFGDVGDALESIRGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRSSSHFVMEVKGDLTAKKWLALLELARQDHGALDCCVVWILSHGCQ 240
DB 181 TGSNIDCEKLRRLRRSSSHFVMEVKGDLTAKKWLALLELARQDHGALDCCVVWILSHGCQ 240
QY 241 ASHLQFPAGVGTGDCPVSVSEKI VNIENGTS CP SLGGKPKLFFFIQACGGEQKDHGFEVAS 300

DB 241 ASHLQFPAGVGTGDCPVSVSEKI VNIENGTS CP SLGGKPKLFFFIQACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDAILSLPTPSDIFVSYSTFPFVSVWRDPKSG 360
DB 301 TSPDESFGSNPEPDATPFQEGRLTFDQDAILSLPTPSDIFVSYSTFPFVSVWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKKLLFFKTS 416
DB 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKKLLFFKTS 416

RESULT 5

US-09-227-721-30

; Sequence 30, Application US/09227721

; Patent No. 6379950

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 480140.431

; CURRENT APPLICATION NUMBER: US/09/227,721

; CURRENT FILING DATE: 1999-01-08

; NUMBER OF SEQ ID NOS: 116

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 30

; LENGTH: 416

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-227-721-30

Query Match 98.9%; Score 2157; DB 4; Length 416;
Best Local Similarity 99.0%; Pred. No. 1.7e-227;
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 60
DB 1 MDEADRLRLRCRLRLVEELQVDQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 60
QY 61 DLETRGSQLPLFTISCLDTCQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 120
DB 61 DLETRGSQLPLFTISCLDTCQDMLASFLRNQAGKLSKPTLENLTVPVLRPEIRKPEV 120
QY 121 LRPETPRVDIGSGGFGDVGDALESIRGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
DB 121 LRPETPRVDIGSGGFGDVGDALESIRGNADLAYILSMPCGHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRSSSHFVMEVKGDLTAKKWLALLELARQDHGALDCCVVWILSHGCQ 240
DB 181 TGSNIDCEKLRRLRRSSSHFVMEVKGDLTAKKWLALLELARQDHGALDCCVVWILSHGCQ 240
QY 241 ASHLQFPAGVGTGDCPVSVSEKI VNIENGTS CP SLGGKPKLFFFIQACGGEQKDHGFEVAS 300
DB 241 ASHLQFPAGVGTGDCPVSVSEKI VNIENGTS CP SLGGKPKLFFFIQACGGEQKDHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPFQEGRLTFDQDAILSLPTPSDIFVSYSTFPFVSVWRDPKSG 360
DB 301 TSPDESFGSNPEPDATPFQEGRLTFDQDAILSLPTPSDIFVSYSTFPFVSVWRDPKSG 360
QY 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKKLLFFKTS 416
DB 361 SWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFKKLLFFKTS 416

RESULT 6

US-09-954-697-30

; Sequence 30, Application US/09954697

; Patent No. 6610541

; GENERAL INFORMATION:

; APPLICANT: Alnemri, Emad S.

; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 480140.431D2

; CURRENT APPLICATION NUMBER: US/09/954,697

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; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-30

Query Match      98.9%; Score 2157; DB 4; Length 416;
Best Local Similarity 99.0%; Pred. No. 1.7e-227;
Matches 412; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEQLVDQLWDVLLSRELPRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEQLVDQLWDVLLSSELFRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQLPLFISCLEDTGQDMLASFLRTNRQAKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSQLPLFISCLEDTGQDMLASFLRTNRQAKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 121 LPETPRPVDSGGFGDVGALESIRGNADLAYIILSMPECGHCLIIINNPNFCRESGLRTR 180
Db 121 LPETPRPVDSGGFGDVGALESIRGNADLAYIILSMPECGHCLIIINNPNFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRFSSPHFMEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCG 240
Db 181 TGSNIDCEKLRRLRRFSSPHFMEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCG 240
QY 241 ASHLQFPGAVYTGDCPVSVKIVNIFNGTSCPSLGKPKLFFIQACGGEQKHGFEVAS 300
Db 241 ASHLQFPGAVYTGDCPVSVKIVNIFNGTSCPSLGKPKLFFIQACGGEQKHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPQEGRLTFDQLDAISSLPTSDIFVSYSTFPFGVSWDRPKSG 360
Db 301 TSPDESFGSNPEPDATPQEGRLTFDQLDAISSLPTSDIFVSYSTFPFGVSWDRPKSG 360
QY 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416
Db 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416

RESULT 7
US-09-257-218-2
; Sequence 2, Application US/09257218
; Patent No. 6271361
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/257,218
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-257-218-2

Query Match      98.8%; Score 2153; DB 3; Length 416;
Best Local Similarity 98.8%; Pred. No. 4.8e-227;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEQLVDQLWDVLLSRELPRPHMIEDIQAGSGSRDQARQLII 60
Db 1 MDEADRLRLRCRLRLVEQLVDQLWDVLLSSELFRPHMIEDIQAGSGSRDQARQLII 60
QY 61 DLETRGSQLPLFISCLEDTGQDMLASFLRTNRQAKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSQLPLFISCLEDTGQDMLASFLRTNRQAKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 121 LPETPRPVDSGGFGDVGALESIRGNADLAYIILSMPECGHCLIIINNPNFCRESGLRTR 180
Db 121 LPETPRPVDSGGFGDVGALESIRGNADLAYIILSMPECGHCLIIINNPNFCRESGLRTR 180
QY 181 TGSNIDCEKLRRLRRFSSPHFMEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCG 240
Db 181 TGSNIDCEKLRRLRRFSSPHFMEVKGDLTAKKMWLALLELARQDHGALDCCVVVILSHGCG 240
QY 241 ASHLQFPGAVYTGDCPVSVKIVNIFNGTSCPSLGKPKLFFIQACGGEQKHGFEVAS 300
Db 241 ASHLQFPGAVYTGDCPVSVKIVNIFNGTSCPSLGKPKLFFIQACGGEQKHGFEVAS 300
QY 301 TSPDESFGSNPEPDATPQEGRLTFDQLDAISSLPTSDIFVSYSTFPFGVSWDRPKSG 360
Db 301 TSPDESFGSNPEPDATPQEGRLTFDQLDAISSLPTSDIFVSYSTFPFGVSWDRPKSG 360
QY 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416
Db 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNLRKLPFKTS 416

RESULT 8
US-09-311-760-2
; Sequence 2, Application US/09311760
; Patent No. 6274318
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/311,760
; FILING DATE: 13-May-1999
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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/865,579
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-311-760-2

Query Match          98.8%; Score 2153; DB 3; Length 416;
Best Local Similarity 98.8%; Pred. No. 4.8e-227;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRELLRRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRELLRRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
QY 61 DLETRGSQLPLFTISCLEDTGQDMLASFLRTRNQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSQLPLFTISCLEDTGQDMLASFLRTRNQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 121 LRPEPRPVDIGSGFGDVGALSLRGADLAIYLSMEPCGHCLIIINNVCRESGLRTR 180
Db 121 LRPEPRPVDIGSGFGDVGALSLRGADLAIYLSMEPCGHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRPRSSLHFVVEVKGDLTAKMVLALLELARQDHGALDCCVVVILSHGCG 240
Db 181 TGSNIDCEKLRPRSSLHFVVEVKGDLTAKMVLALLELARQDHGALDCCVVVILSHGCG 240
QY 241 ASHLQFPAGVYGTGDCPVSVKEKIVNIFNGTSCPSLGGKPKLFFIQACGGQKHGFVEAS 300
Db 241 ASHLQFPAGVYGTGDCPVSVKEKIVNIFNGTSCPSLGGKPKLFFIQACGGQKHGFVEAS 300
QY 301 TSPEDSPGNRPDPATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSG 360
Db 301 TSPEDSPGNRPDPATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSG 360
QY 361 SWVYETLDDIFEQWASEDLQSLLLRVANAVSVKGIYKQMPGCNFKLFFKTS 416
Db 361 SWVYETLDDIFEQWASEDLQSLLLRVANAVSVKGIYKQMPGCNFKLFFKTS 416

RESULT 9
US-08-865-579-2
; Sequence 2, Application US/08865579
; Patent No. 6455296
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-865-579-2

Query Match          98.8%; Score 2153; DB 4; Length 416;
Best Local Similarity 98.8%; Pred. No. 4.8e-227;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRELLRRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
Db 1 MDEADRELLRRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQAGSGRRDQARQLII 60
QY 61 DLETRGSQLPLFTISCLEDTGQDMLASFLRTRNQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
Db 61 DLETRGSQLPLFTISCLEDTGQDMLASFLRTRNQAGKLSKPTLENLTPVVLRLPEIRKPEV 120
QY 121 LRPEPRPVDIGSGFGDVGALSLRGADLAIYLSMEPCGHCLIIINNVCRESGLRTR 180
Db 121 LRPEPRPVDIGSGFGDVGALSLRGADLAIYLSMEPCGHCLIIINNVCRESGLRTR 180
QY 181 TGSNIDCEKLRPRSSLHFVVEVKGDLTAKMVLALLELARQDHGALDCCVVVILSHGCG 240
Db 181 TGSNIDCEKLRPRSSLHFVVEVKGDLTAKMVLALLELARQDHGALDCCVVVILSHGCG 240
QY 241 ASHLQFPAGVYGTGDCPVSVKEKIVNIFNGTSCPSLGGKPKLFFIQACGGQKHGFVEAS 300
Db 241 ASHLQFPAGVYGTGDCPVSVKEKIVNIFNGTSCPSLGGKPKLFFIQACGGQKHGFVEAS 300
QY 301 TSPEDSPGNRPDPATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSG 360
Db 301 TSPEDSPGNRPDPATPFQEGRLTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSG 360
QY 361 SWVYETLDDIFEQWASEDLQSLLLRVANAVSVKGIYKQMPGCNFKLFFKTS 416
Db 361 SWVYETLDDIFEQWASEDLQSLLLRVANAVSVKGIYKQMPGCNFKLFFKTS 416

RESULT 10
US-10-059-749-2
; Sequence 2, Application US/10059749
; Patent No. 6566505
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
```

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-059-749-2

Query Match 98.8%; Score 2153; DB 4; Length 416;
Best Local Similarity 98.8%; Pred. No. 4.8e-227;
Matches 411; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDEADRLRLRRLRVEQLVDQLWDVLLSRLRPHMIEDIORAGSSREDQARQLII 60
Db 1 MDEADRLRLRRLRVEQLVDQLWDVLLSRLRPHMIEDIORAGSSREDQARQLII 60

QY 61 DLETRGSQALPLFISCLEPTGDMLASFLRTNRQAKLSKPTLENLTPVLRPEIRKPEV 120
Db 61 DLETRGSQALPLFISCLEPTGDMLASFLRTNRQAKLSKPTLENLTPVLRPEIRKPEV 120

QY 121 LRPETRPVDTGSGFDVGALSRGNADLAYILSMPEPCGCHLIINNVPFCRESGLRTR 180
Db 121 LRPETRPVDTGSGFDVGALSRGNADLAYILSMPEPCGCHLIINNVPFCRESGLRTR 180

QY 181 TGSNIDCKLRFRFSLHFMVKGDLTAKMVLALLLRLARODHGLDCCVVVILSHGCG 240
Db 181 TGSNIDCKLRFRFSLHFMVKGDLTAKMVLALLLRLARODHGLDCCVVVILSHGCG 240

QY 241 ASHLQFPGAVYGTDCGCVSVEKIVNFNGTSCPSLGGKPKLFFIQACGGEQKHGFVEAS 300
Db 241 ASHLQFPGAVYGTDCGCVSVEKIVNFNGTSCPSLGGKPKLFFIQACGGEQKHGFVEAS 300

QY 301 TSPDESPGSNPEPATPFQEGRLTFDQLDAISSLPTSDIFVSYSTPFGFVSWDRDPKSG 360
Db 301 TSPDESPGSNPEPATPFQEGRLTFDQLDAISSLPTSDIFVSYSTPFGFVSWDRDPKSG 360

QY 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKMPCCFNFLRKLFFKTS 416
Db 361 SWYVETLDDIFQWAHSEDLQSLLLRVANAVSVKGIYKMPCCFNFLRKLFFKTS 416

RESULT 11
US-08-852-936C-4
; Sequence 4, Application US/08852936C
; Patent No. 6010878
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.
; APPLICANT: RUBEN, STEVEN M.
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
; TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
; NUMBER OF SEQUENCES: 11
```

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,936C
; FILING DATE: 08-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/018,961
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: 60/020,344
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: 60/017,949
; FILING DATE: 20-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: P50483-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-852-936C-4

Query Match 49.7%; Score 1083; DB 3; Length 203;
Best Local Similarity 100.0%; Pred. No. 2.8e-110;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 MVLLALLEARODHGLDCCVVVILSHGCGASHLQFPGAVYGTDCGCVSVEKIVNFNGTS 271
Db 1 MVLLALLEARODHGLDCCVVVILSHGCGASHLQFPGAVYGTDCGCVSVEKIVNFNGTS 60

QY 272 CPSLGGKPKLFFIQACGGEQKHGFVEASTSPDES PGSNPEPATPFQEGRLTFDQLDA 331
Db 61 CPSLGGKPKLFFIQACGGEQKHGFVEASTSPDES PGSNPEPATPFQEGRLTFDQLDA 120

QY 332 ISSLPTSDIFVSYSTPFGFVSWDRDPKSGSWYVETLDDIFQWAHSEDLQSLLLRVANAV 391
Db 121 ISSLPTSDIFVSYSTPFGFVSWDRDPKSGSWYVETLDDIFQWAHSEDLQSLLLRVANAV 180

QY 392 SVKGIYKMPCCFNFLRKLFF 413
Db 181 SVKGIYKMPCCFNFLRKLFF 202

RESULT 12
US-09-300-328-4
; Sequence 4, Application US/09300328
; Patent No. 6294169
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: HE, WEI-WU
; APPLICANT: KIKLY, KRISTINE K.
; APPLICANT: RUBEN, STEVEN M.
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING
; TITLE OF INVENTION: ENZYME LIKE APOPTOTIC PROTEASE-6
; NUMBER OF SEQUENCES: 11
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;
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,308
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: NORTH, ROBERT J
; REGISTRATION NUMBER: 27,366
; REFERENCE/DOCKET NUMBER: 19840 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-7262
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-964-308-6

Query Match          19.2%; Score 418; DB 3; Length 277;
Best Local Similarity 33.2%; Pred. No. 3.6e-37;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAYILSEPCGHCLIIINNVPFCRSGGLRTGSGNIDCEKLRFRFSSLHFMVEVKGDLTA 209
Db 34 DNSYKMDYPMGLCIIINNKNFKHKTGTSRSGTDVDAANLRETFRNLKYEVRNKNDLTR 93

QY 210 KMWLALLELARQDHGALDCCVVVILSHGCOASHLQFPFVAVYGTGDCPVSVEKIVNIENG 269
Db 94 EEIVELMRDVSKEHDSKRSSFVCVLLSHGEE-----GIIFGTNG-PVDLKKIITNFRFG 145

QY 270 TSCPSLGGPKPLFFITQACGGEQKHGFVASTSPDESGFSGNPEPDATPFQEGLTFDQL 329
Db 146 DRCRSLTGKPKLFIQACRGTELDGCIETDSGVDDM----- 182

QY 330 DAISLPTSPDIFVSYSTFPFVSWRDPKSGSWYVETLDDIFEQWASEDLQSLLRVAN 389
Db 193 -ACHKIPVEADFLYAYSTAGYYSWRNSKGSWFIQSLCAMLKQYADKLEPFMHILTRVNR 241

QY 390 AVSVK-----GIYKMPGCFNFKLFF 413
Db 242 KVATFESFSDATFHAKKQIPCIIVSMLTKELYF 275
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RESULT 15
US-08-462-969B-4
; Sequence 4, Application US/08462969B
; Patent No. 6087150
; GENERAL INFORMATION:
; APPLICANT: He, Wei-Wu et al.
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
; TITLE OF INVENTION: Like Apoptosis Protease 3 and 4
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Ave.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,969B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/334,251
; FILING DATE: 11-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF140P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-462-969B-4

Query Match          19.2%; Score 418; DB 3; Length 277;
Best Local Similarity 33.2%; Pred. No. 3.6e-37;
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 150 DLAYILSEPCGHCLIIINNVPFCRSGGLRTGSGNIDCEKLRFRFSSLHFMVEVKGDLTA 209
Db 34 DNSYKMDYPMGLCIIINNKNFKHKTGTSRSGTDVDAANLRETFRNLKYEVRNKNDLTR 93

QY 210 KMWLALLELARQDHGALDCCVVVILSHGCOASHLQFPFVAVYGTGDCPVSVEKIVNIENG 269
Db 94 EEIVELMRDVSKEHDSKRSSFVCVLLSHGEE-----GIIFGTNG-PVDLKKIITNFRFG 145

QY 270 TSCPSLGGPKPLFFITQACGGEQKHGFVASTSPDESGFSGNPEPDATPFQEGLTFDQL 329
Db 146 DRCRSLTGKPKLFIQACRGTELDGCIETDSGVDDM----- 182

QY 330 DAISLPTSPDIFVSYSTFPFVSWRDPKSGSWYVETLDDIFEQWASEDLQSLLRVAN 389
Db 193 -ACHKIPVEADFLYAYSTAGYYSWRNSKGSWFIQSLCAMLKQYADKLEPFMHILTRVNR 241

QY 390 AVSVK-----GIYKMPGCFNFKLFF 413
Db 242 KVATFESFSDATFHAKKQIPCIIVSMLTKELYF 275
```

Search completed: August 3, 2004, 09:03:39
Job time : 20 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 09:07:32 ; Search time 17 Seconds
(without alignments)
2353.863 Million cell updates/sec

Title: US-09-961-201a-1
Perfect score: 416
Sequence: 1 MDEADRLRLRCRLRLVEEL.....YKMPGCFNLRKXLFKTS 416

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : PIR 78:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	416	100.0	416	2	G02635
2	28	6.7	454	2	JC7123
3	9	2.2	370	2	B88455
4	9	2.2	1196	2	T09356
5	8	1.9	232	2	A69501
6	8	1.9	324	2	AE3650
7	8	1.9	368	2	T36004
8	8	1.9	372	2	G82328
9	8	1.9	579	2	T45344
10	8	1.9	752	2	T16508
11	8	1.9	787	2	T16800
12	8	1.9	787	2	T00798
13	8	1.9	794	2	T23048
14	8	1.9	1393	2	E72122
15	8	1.9	1393	2	B86501
16	8	1.9	1397	2	E81548
17	7	1.7	98	2	AE2465
18	7	1.7	132	2	T44759
19	7	1.7	135	2	B49218
20	7	1.7	173	2	H90776
21	7	1.7	180	2	D86609
22	7	1.7	180	2	E72014
23	7	1.7	180	2	F71056
24	7	1.7	182	2	D75088
25	7	1.7	182	2	G71411
26	7	1.7	186	2	F75396
27	7	1.7	189	2	F82448
28	7	1.7	200	2	G82270
29	7	1.7	206	2	AF2299

30	7	1.7	224	2	B83859	hypothetical prote
31	7	1.7	234	2	T51025	hypothetical prote
32	7	1.7	236	2	T13312	hypothetical prote
33	7	1.7	237	2	G84678	probable RING zinc
34	7	1.7	240	2	D87435	transcription regu
35	7	1.7	241	2	H72591	probable hexulose-
36	7	1.7	247	2	C82995	two-component resp
37	7	1.7	261	2	E69455	conserved hypotet
38	7	1.7	262	2	T18886	hypothetical prote
39	7	1.7	267	2	T06613	hypothetical prote
40	7	1.7	274	2	JQ0886	nosinepride resist
41	7	1.7	276	2	T36288	probable ABC-type
42	7	1.7	276	2	E87682	methyltransferase,
43	7	1.7	285	2	B97536	ATP/GTP-binding pr
44	7	1.7	294	2	G71276	conserved hypotet
45	7	1.7	306	2	JC1120	sdsB protein - Pse
46	7	1.7	307	2	D75447	ABC transporter, A
47	7	1.7	311	1	G64456	conserved hypotet
48	7	1.7	313	2	S60713	polygalacturonase-
49	7	1.7	318	2	AB0350	probable membrane
50	7	1.7	319	2	A72637	hypothetical prote
51	7	1.7	323	2	G83461	hypothetical prote
52	7	1.7	323	2	T30513	hypothetical prote
53	7	1.7	333	2	AH0272	conserved hypotet
54	7	1.7	336	2	AF2085	transcription regu
55	7	1.7	345	2	H72488	probable anthranil
56	7	1.7	349	2	AC0856	conserved hypotet
57	7	1.7	358	2	H71058	hypothetical prote
58	7	1.7	358	2	H90052	conserved hypotet
59	7	1.7	360	2	AB3004	conserved hypotet
60	7	1.7	361	2	B70189	rod shape-determin
61	7	1.7	379	2	H87268	hypothetical prote
62	7	1.7	388	2	G90450	hypothetical prote
63	7	1.7	390	2	D82186	beta-lactamase-rel
64	7	1.7	397	2	T23026	hypothetical prote
65	7	1.7	401	2	S59670	RAD17 protein - ye
66	7	1.7	404	2	S45923	probable phosphop
67	7	1.7	420	2	A47649	probable inner mem
68	7	1.7	420	2	E95982	probable transport
69	7	1.7	444	2	AC2755	GTP-binding protel
70	7	1.7	487	1	VZEBPT	sensor kinase phoQ
71	7	1.7	487	2	AG0646	sensor protein pho
72	7	1.7	496	2	F84664	hypothetical prote
73	7	1.7	505	1	S77034	protein kinase pkn
74	7	1.7	505	2	AC3361	GTP-binding protei
75	7	1.7	508	2	B81212	fatty acid efflux

ALIGNMENTS

RESULT 1
G02635
ICE-LAP6 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C:Accession: G02635
R:Duan, H.; Orth, K.; Chinnaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.; Dixit,
submitted to the EMBL Data Library, April 1996
A:Reference number: H01513
A:Accession: G02635
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-416 <DUA>
A:Cross-references: EMBL:U56390; NID:gl336026; PTDN:AAC50640.1; PID:gl336027

Query Match 100.0%; Score 416; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDEADRLRLRCRLRLVEELQVDQMDVLLSRLFRPHMIEDIQAGSGSRDQARQLII 60
DB 1 MDEADRLRLRCRLRLVEELQVDQMDVLLSRLFRPHMIEDIQAGSGSRDQARQLII 60

QY 61 DLETRGSQLPLPISCLDTCQDMLASFLTRNQAGKLSKPTLENLTPVVLRIPEIRKEV 120
Db 61 DLETRGSQLPLPISCLDTCQDMLASFLTRNQAGKLSKPTLENLTPVVLRIPEIRKEV 120
QY 121 LRPEPRPVDIGSGFGDVGALSLRGNADLAYILSMPECHCLIIINNVPFCRESGLRTR 180
Db 121 LRPEPRPVDIGSGFGDVGALSLRGNADLAYILSMPECHCLIIINNVPFCRESGLRTR 180
QY 181 TGSNIDCEKLRFRPSSLHFVVEVKGDLTAKQWLVALLLELARAQDHGALDCCVWVILSHGCQ 240
Db 181 TGSNIDCEKLRFRPSSLHFVVEVKGDLTAKQWLVALLLELARAQDHGALDCCVWVILSHGCQ 240
QY 241 ASHLQFPGAVYGTDCPVSEKIVINIFNGTSCPSLGGKPKLFFFOACGGEQKHGFEVAS 300
Db 241 ASHLQFPGAVYGTDCPVSEKIVINIFNGTSCPSLGGKPKLFFFOACGGEQKHGFEVAS 300
QY 301 TSPDESPGNSPEPDATPFQEGRLTFQQLDAISSLPTPSDIFVSYSTFPFGVSWRDPKSG 360
Db 301 TSPDESPGNSPEPDATPFQEGRLTFQQLDAISSLPTPSDIFVSYSTFPFGVSWRDPKSG 360
QY 361 SWYVETLDDIPEQWAHSEDQLSLLLRVANAVSVKGIYQKMPGCFNFKKLPFFKTS 416
Db 361 SWYVETLDDIPEQWAHSEDQLSLLLRVANAVSVKGIYQKMPGCFNFKKLPFFKTS 416

RESULT 2

JC7123
caspase-9 long chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C:Accession: JC7123
R:Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264, 550-555, 1999
A:Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9.
A:Reference number: JC7123; MUID:20001956; PMID:10529400
A:Accession: JC7123
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-454 <FOU>
A:Cross-references: DDBJ:AB019600; NID:g6440941; PID:g6440942

Query Match 6.7%; Score 28; DB 2; Length 454;
Best Local Similarity 100.0%; Pred. No. 5.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 CPSLGGKPKLFFIOACGGEQKHGFEVA 299
Db 310 CPSLGGKPKLFFIOACGGEQKHGFEVA 337

RESULT 3

B88455
protein T15B12.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: B88455
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2103, 1999.
A:Accession: B88455
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-370 <STO>
A:Cross-references: GB:chr_III; PID:AAA21560.1; PID:g540264; GSPDB:GN00021; CBSP:T15B12
C:Genetics:
A:Gene: T15B12.2
A:Map position: 3

Query Match 2.2%; Score 9; DB 2; Length 370;

Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 131 IGSGGFGDV 139
Db 57 IGSGGFGDV 65

RESULT 4

T09356
brassinosteroid-insensitive protein BRI1 - Arabidopsis thaliana
N:Alternate names: protein F23K16.30
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 24-Nov-1999
C:Accession: T09356
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z16652
A:Accession: T09356
A:Molecule type: DNA
A:Residues: 1-1196 <BEV>
A:Cross-references: EMBL:AL078620; GSPDB:GN00062; ATSP:F23K16.30
A:Experimental source: cultivar Columbia; BAC clone F23K16
C:Genetics:
A:Gene: ATSP:F23K16.30; BRI1
A:Map position: 4
C:Superfamily: protein kinase Xa21; leucine-rich alpha-2-glycoprotein repeat homology;

Query Match 2.2%; Score 9; DB 2; Length 1196;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 IGSGGFGDV 139
Db 889 IGSGGFGDV 897

RESULT 5

A69501
hypothetical protein AF2010 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000
C:Accession: A69501
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: A69501
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-232 <KLE>
A:Cross-references: GB:AF000964; GB:AF000782; NID:g2689287; PIDN:AAB89255.1; PID:g264955
C:Superfamily: Archaeoglobus fulgidus hypothetical protein AF2010

Query Match 1.9%; Score 8; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 ESSLRTTRT 181
Db 29 ESSLRTTRT 36

RESULT 6

A83650
oxidoreductase (EC 1.1.1.-) [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: A83650

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, E.; Mazur, M.; Gotsman, E.; Selkov, E.; Elzer, P.H.; Hagijs, S.; O'Callaghan, D.; Letessier, A.; et al. Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melitens*

A:Reference number: AD3252; PMID:11756688

A:Accession: AE3650

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-324 <KUR>

A:Cross-references: GB:AE008918; PIDN:AA154368.1; PID:gl17985352; GSPDB:GN00191

A:Experimental source: strain 16M

C:Genetics:

A:Map position: II

C:Keywords: oxidoreductase

Query Match 1.9%; Score 8; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 ALLELARQ 222
|||||
Db 103 ALLELARQ 110

RESULT 7

T36004

hypothetical protein SCC22.14c - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 08-Sep-2000

C:Accession: T36004

R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999

A:Reference number: Z21574

A:Accession: T36004

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-368 <SEE>

A:Cross-references: EMBL:AL096839; PIDN:CAB50757.1; GSPDB:GN00070; SCOEDB:SCC22.14c

C:Genetics:

A:Gene: SCOEDB:SCC22.14c

C:Superfamily: Streptomyces coelicolor hypothetical protein SCC22.14c

Query Match 1.9%; Score 8; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EADRRLLR 10
|||||
Db 81 EADRRLLR 88

RESULT 8

G82328

aminotransferase, class V VC0392 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)

C:Species: *Vibrio cholerae*

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: G82328

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; et al. Nature 406, 477-483, 2000

A:Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: G82328

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-372 <HEI>

A:Cross-references: GB:AE004127; GB:AE003852; NID:g9654808; PIDN:AAF93565.1; GSPDB:GN001

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC0392

A:Map position: 1

C:Superfamily: serine-pyruvate aminotransferase

Query Match 1.9%; Score 8; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 GCFVSVEK 262
|||||
Db 119 GCFVSVEK 126

RESULT 9

T45344

hypothetical protein MLCB57.28c [imported] - *Mycobacterium leprae*

C:Species: *Mycobacterium leprae*

C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 28-Jul-2000

C:Accession: T45344

R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, September 1997

A:Reference number: Z16918

A:Accession: T45344

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-579 <PAR>

A:Cross-references: EMBL:Z99494; PIDN:CAB16668.1

A:Experimental source: cosmid B57

C:Genetics:

A:Note: MLCB57.28c

C:Superfamily: *Mycobacterium leprae* hypothetical protein MLCB57.28c

Query Match 1.9%; Score 8; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 GLRTRTGS 183
|||||
Db 17 GLRTRTGS 24

RESULT 10

T16508

hypothetical protein F59A6.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16508

R;Nhan, M. submitted to the EMBL Data Library, December 1995

A:Description: the sequence of C. elegans cosmid F59A6.

A:Reference number: Z18526

A:Accession: T16508

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-752 <NHA>

A:Cross-references: EMBL:U41994; NID:gl123047; PID:gl123051; PIDN:AAA83455.1; CESP:F59A6

C:Genetics:

A:Gene: CESP:F59A6.4

A:Introns: 43/3; 146/3; 334/1; 400/3; 433/2; 515/3; 672/1

Query Match 1.9%; Score 8; DB 2; Length 752;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 GSGGFGDV 139
|||||
Db 441 GSGGFGDV 448

RESULT 11

T16800

hypothetical protein T05A7.6 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C;Accession: T16800
 R;Chisoe, S.
 Submitted to the EMBL Data Library, November 1995
 A;Description: The sequence of C. elegans cosmid T05A7.
 A;Reference number: Z18580
 A;Accession: T16800
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-758 <CHI>
 A;Cross-references: EMBL:U40028; NID:g1055143; PID:g1055145; PIDN:AAA81115.1; CESP:T05A7
 C;Genetics:
 A;Gene: CESP:T05A7.6
 A;Introns: 41/3; 142/3; 330/1; 396/3; 439/2; 678/1

Query Match 1.9%; Score 8; DB 2; Length 758;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 GSGGFGDV 139
 Db 447 GSGGFGDV 454
 |||||

RESULT 12
 T00798
 hypothetical protein At2g32700 [imported] - Arabidopsis thaliana
 N;Alternate names: hypothetical protein F24L7.16
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001
 C;Accession: T00798; D84736
 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
 submitted to the EMBL Data Library, February 1998
 A;Description: Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence.
 A;Reference number: Z14204
 A;Accession: T00798
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-787 <ROU>
 A;Cross-references: EMBL:AC003974; NID:g2914688; PID:g2914703
 A;Experimental source: cultivar Columbia
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: D84736
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-787 <STO>
 A;Cross-references: GB:AE002093; NID:g2914703; PIDN:AAC04493.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g32700; F24L7.16
 A;Map position: 2
 A;Introns: 11/2; 44/1; 80/3; 174/2; 200/3; 238/1; 254/3; 347/3; 372/3; 448/3; 497/1; 533

Query Match 1.9%; Score 8; DB 2; Length 787;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 FGDVGALE 143
 Db 456 FGDVGALE 463
 |||||

RESULT 13
 T23048
 hypothetical protein H05L14.1 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C;Accession: T23048; T25112
 R;Barlow, K.
 submitted to the EMBL Data Library, October 1997

A;Reference number: Z19662
 A;Accession: T23048
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-794 <WIL>
 A;Cross-references: EMBL:Z99772; PIDN:CAB16921.1; GSPDB:GN00019; CESP:H05L14.1
 A;Experimental source: clone H05L14
 R;McMurray, A.
 submitted to the EMBL Data Library, June 1996
 A;Reference number: Z19982
 A;Accession: T25112
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-794 <WT2>
 A;Cross-references: EMBL:Z75550; PIDN:CAA99932.1; GSPDB:GN00019; CESP:H05L14.1
 A;Experimental source: clone T22C1
 C;Genetics:
 A;Gene: CESP:H05L14.1
 A;Map position: 1
 A;Introns: 8/1; 61/3; 147/3; 196/3; 231/3; 354/1; 383/2; 437/2; 584/3; 635/3; 658/3; 70

Query Match 1.9%; Score 8; DB 2; Length 794;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 GSGGFGDV 139
 Db 468 GSGGFGDV 475
 |||||

RESULT 14
 E72122
 RNA polymerase beta' - Chlamydomophila pneumoniae (strain CWL029)
 C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
 C;Accession: E72122
 R;Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.
 Nature Genet. 21, 385-389, 1999
 A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
 A;Reference number: A72000; MUID:99206606; PMID:10192388
 A;Accession: E72122
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1393 <ARN>
 A;Cross-references: GB:AE001593; GB:AE001363; NID:g4376334; PIDN:AAD18235.1; PID:g43763
 A;Experimental source: strain CWL029
 C;Genetics:
 A;Gene: rpoC
 C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match 1.9%; Score 8; DB 2; Length 1393;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 377 SEDLQSL 384
 Db 194 SEDLQSL 201
 |||||

RESULT 15
 B86501
 RNA polymerase beta' [imported] - Chlamydomophila pneumoniae (strain J138)
 C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C;Accession: B86501
 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I
 Nucleic Acids Res. 28, 2311-2314, 2000
 A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A;Reference number: A86491; MUID:20330349; PMID:10871362
 A;Accession: B86501
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1393 <STO>

A;Cross-references: GB:BA000008; NID:g8978455; PIDN:BAA98292.1; GSPDB:GN00142
 A;Experimental source: strain J138
 C;Genetics:

C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match 1.9%; Score 8; DB 2; Length 1393;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 SEDLQSL 384
 |||||
 Db 194 SEDLQSL 201

RESULT 16

E81548
 DNA-directed RNA polymerase, beta' chain CP0693 [imported] - Chlamydophila pneumoniae (s
 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
 C;Accession: E81548

R;Read, I.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
 C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: E81548

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1397 <REA>

A;Cross-references: GB:AE002228; GB:AE002161; NID:g7189606; PIDN:AAF38501.1; PID:g718960

A;Experimental source: strain AR39, HL cells

C;Genetics:

A;Gene: CP0693

C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match 1.9%; Score 8; DB 2; Length 1397;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 SEDLQSL 384
 |||||
 Db 198 SEDLQSL 205

RESULT 17

AE2465
 HicA protein [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C;Accession: AE2465

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AE2465

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-98 <KUR>

A;Cross-references: GB:BA000019; PIDN:BA876976.1; PID:gl7134416; GSPDB:GN00179

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: asl5277

Query Match 1.7%; Score 7; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 TLDDIFE 372
 |||||
 Db 10 TLDDIFE 16

RESULT 18

T44759

glycine cleavage system protein H [imported] - Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 04-Mar-2000

C;Accession: T44759

R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, October 1997

A;Reference number: Z22833

A;Accession: T44759

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-132 <PAR>

A;Cross-references: EMBL:AL008609; PIDN:CAA15469.1

A;Experimental source: cosmid B1788

C;Genetics:

A;Gene: gcvH

C;Superfamily: glycine cleavage system protein H; lipoyl/biotin-binding homology

Query Match 1.7%; Score 7; DB 2; Length 132;

Best Local Similarity 100.0%; Pred. No. 48;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 DVGAL 144
 |||||
 Db 109 DVGAL 115

RESULT 19

B49218

hemagglutinin homolog pmGAI.3 - Mycoplasma gallisepticum (fragment)

C;Species: Mycoplasma gallisepticum

C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 07-Dec-1999

C;Accession: B49218

R;Markham, P.F.; Glew, M.D.; Whithear, K.G.; Walker, I.D.

Infect. Immun. 61, 903-909, 1993

A;Title: Molecular cloning of a member of the gene family that encodes pmGA, a hemagglut

A;Reference number: A49218; MUID:93162830; PMID:8432610

A;Accession: B49218

A;Status: preliminary

A;Molecule type: DNA; protein

A;Residues: 1-135 <MAR>

A;Cross-references: GB:S55216; NID:g265625; PIDN:AAB25398.1; PID:g265627

A;Experimental source: S6

A;Note: sequence extracted from NCBI backbone (NCBIN:125182, NCBIP:125184)

C;Genetics:

A;Genetic code: SGC3

Query Match 1.7%; Score 7; DB 2; Length 135;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 TLENLTP 108
 |||||
 Db 129 TLENLTP 135

RESULT 20

H90776

hypothetical protein ECs1184 [imported] - Escherichia coli (strain O157:H7, substrain RH

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

C;Accession: H90776

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Iihii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: H90776

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-173 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34607.1; PID:q13360644; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RMD 050952
C;Genetics:
A;Gene: ECs1184

Query Match 1.7%; Score 7; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 PVWLPE 114
Db 134 PVWLPE 140

RESULT 21

peptidyl tRNA hydrolase [imported] - Chlamydomophila pneumoniae (strain J138)

C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C;Accession: D86609

R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise

Nucleic Acids Res. 28, 2311-2314, 2000

A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A;Reference number: A86491; MUID:20330349; PMID:10871362

A;Accession: D86609

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-180 <STO>

A;Cross-references: GB:BA000008; NID:98979324; PIDN:BAA99158.1; GSPDB:GN00142

A;Experimental source: strain J138

C;Genetics:

A;Gene: pth

C;Superfamily: peptidyl-tRNA hydrolase

Query Match 1.7%; Score 7; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 RLVEELQ 21
Db 29 RLVEELQ 35

RESULT 22

peptidyl-tRNA hydrolase CP0909 [imported] - Chlamydomophila pneumoniae (strains CWL029 and

C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000

C;Accession: E72014; G81523

R;Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999

A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A;Reference number: A72000; MUID:99206606; PMID:10192388

A;Accession: E72014

A;Molecule type: DNA

A;Residues: 1-180 <ARN>

A;Cross-references: GB:AE001675; GB:AE001363; NID:g4377273; PIDN:AAD19088.1; PID:g437727

A;Experimental source: strain CWL029

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: G81523

A;Molecule type: DNA

A;Residues: 1-180 <REA>

A;Cross-references: GB:AE002250; GB:AE002161; NID:g7189821; PIDN:AAF38694.1; PID:g718982

A;Experimental source: strain AR39, HL cells

C;Genetics:

A;Gene: pth; CP0909

C;Superfamily: peptidyl-tRNA hydrolase

Query Match 1.7%; Score 7; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 RLVEELQ 21
Db 29 RLVEELQ 35

RESULT 23

F71056

hypothetical protein PH1148 - Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000

C;Accession: F71056

R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kuhida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic

A;Reference number: A71000; MUID:98344137; PMID:9679194

A;Accession: F71056

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-180 <KAW>

A;Cross-references: GB:AP000005; NID:g3236132; PIDN:BAA30248.1; PID:g3257565

A;Experimental source: strain OT3

A;Note: this accession replaces an interim accession for a sequence replaced by GenBank

C;Genetics:

A;Gene: PH1148

Query Match 1.7%; Score 7; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 215 ALLELAR 221
Db 174 ALLELAR 180

RESULT 24

D75088

hypothetical protein PAB0726 - Pyrococcus abyssi (strain Orsay)

C;Species: Pyrococcus abyssi

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C;Accession: D75088

R;anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str

A;Reference number: A75001

A;Accession: D75088

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-182 <KAW>

A;Cross-references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB50009.1; PID:g545836

A;Experimental source: strain Orsay

C;Genetics:

A;Gene: PAB0726

Query Match 1.7%; Score 7; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 215 ALLELAR 221
Db 176 ALLELAR 182

RESULT 25

G71411

hypothetical protein - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cross)

A;Variety: columbia

C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998

C;Accession: G71411
 R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirkx, P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Fohl, T.M.; Terryn, N.; Gielavanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Nature 391, 485-488, 1998
 A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans C.; Chalwatzis, N.
 A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thaliana
 A;Reference number: A71400; MUID:96121113; PMID:9461215
 A;Accession: G71411
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-182 <BEV>
 A;Cross-references: GB:297337; NID:g2244829; PID:e326833; PID:g2244843
 C;Genetics:
 A;Map position: 4COP9-4G3845

Query Match 1.7%; Score 7; DB 2; Length 182;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 405 NFLRKXL 411
 |||||
 Db 3 NFLRKXL 9

RESULT 26
 S73396
 hypothetical protein c04030 - Sulfolobus solfataricus
 C;Species: Sulfolobus solfataricus
 C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 17-Mar-1999
 C;Accession: S75396
 R;Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S. Mol. Microbiol. 22, 175-191, 1996
 A;Title: Organizational characteristics and information content of an archaeal genome: 1
 A;Reference number: S73076; MUID:97055432; PMID:8999719
 A;Accession: S75396
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-186 <SEN>
 A;Cross-references: EMBL:Y08257; NID:g1707772; PID:e283882; PID:g1707802
 A;Experimental source: strain P2
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996

Query Match 1.7%; Score 7; DB 2; Length 186;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 LFIISCLE 78
 |||||
 Db 42 LFIISCLE 48

RESULT 27
 F82448
 conserved hypothetical protein VCA0539 [imported] - Vibrio cholerae (strain N16961 serog C;Species: Vibrio cholerae
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Accession: F82448
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-189 <HEI>
 A;Cross-references: GB:AE004384; GB:AE003853; NID:g9657936; PIDN:AAF96441.1; GSPDB:GN001
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:

A;Gene: VCA0539
 A;Map position: 2

Query Match 1.7%; Score 7; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 EVKGDLT 208
 |||||
 Db 121 EVKGDLT 127

RESULT 28

G82270
 hypothetical protein VC0859 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
 C;Species: Vibrio cholerae
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C;Accession: G82270
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Accession: G82270
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-200 <HEI>
 A;Cross-references: GB:AE004171; GB:AE003852; NID:g9655308; PIDN:AAF94021.1; GSPDB:GN001
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:
 A;Gene: VC0859
 A;Map position: 1

Query Match 1.7%; Score 7; DB 2; Length 200;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 EDIQRAG 47
 |||||
 Db 67 EDIQRAG 73

RESULT 29

AF2299
 cobalt transport ATP-binding protein cbiO [imported] - Nostoc sp. (strain PCC 7120)
 C;Species: Nostoc sp. PCC 7120
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C;Accession: AF2299
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A;Reference number: AB1807; MUID:21595285; PMID:11759840
 A;Accession: AF2299
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-206 <KUR>
 A;Cross-references: GB:BA000019; PIDN:BA075648.1; PID:g17133083; GSPDB:GN00179
 A;Experimental source: strain PCC 7120
 C;Genetics:
 A;Gene: cbiO
 C;Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 1.7%; Score 7; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 RDOARQL 58
 |||||
 Db 83 RDOARQL 89

```

RESULT 30
E83859
hypothetical protein BH1677 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: E83859
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: E83859
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-224 <STO>
A:Cross-references: GB:AP001512; GB:BA000004; NID:gl0174030; PIDN:BA05396.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1677
C:Superfamily: conserved hypothetical protein TM1511
Query Match 1.7%; Score 7; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 215 ALLELAR 221
| | | | |
Db 207 ALLELAR 213

RESULT 31
T51025
hypothetical protein B7F21.60 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 08-Sep-2000
C:Accession: T51025
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, July 2000
A:Reference number: Z25286
A:Accession: T51025
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-234 <SCH>
A:Cross-references: EMBL:AL389901; GSPDB:GN00116; NCSP:B7F21.60
A:Experimental source: BAC clone B7F21; strain OR74A
C:Genetics:
A:Gene: NCSP:B7F21.60
A:Map position: 6
A:Introns: 16/1; 55/2; 70/3; 129/2; 179/3; 196/1
C:Superfamily: Neurospora crassa hypothetical protein B7F21.60
Query Match 1.7%; Score 7; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 94 QAGKLSK 100
| | | | |
Db 137 QAGKLSK 143

RESULT 32
T13312
hypothetical protein 23 - Streptococcus phage phi-O1205
C:Species: Streptococcus phage phi-O1205
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 18-Aug-2000
C:Accession: T13312
R:Stanley, E.; Fitzgerald, G.F.; Le Marrec, C.; Fayard, B.; van Sinderen, D.
Microbiology 143, 3417-3429, 1997
A:Title: Sequence analysis and characterization of phi O1205, a temperate bacteriophage
A:Reference number: Z17654; MUID:98048466; PMID:9387220
A:Accession: T13312
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA

```

```

A:Residues: 1-236 <STA>
A:Cross-references: EMBL:U88974; NID:g2444080; PID:g2444103; PIDN:AAC79539.1
A:Experimental source: host Streptococcus thermophilus strain CNRZ1205
C:Superfamily: Streptococcus phage phi-O1205 hypothetical protein 23
Query Match 1.7%; Score 7; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 LLSRELF 35
| | | | |
Db 177 LLSRELF 183

RESULT 33
G84678
probable RING zinc finger protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: G84678
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84678
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-237 <STO>
A:Cross-references: GB:AF002093; NID:g4510422; PIDN:AD21508.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g27940
A:Map position: 2
Query Match 1.7%; Score 7; DB 2; Length 237;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 285 QACGGEQ 291
| | | | |
Db 14 QACGGEQ 20

RESULT 34
DB7435
transcription regulator, AraC family [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: DB7435
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kold
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: DB7435
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-240 <STO>
A:Cross-references: GB:AE005673; NID:gl3422878; PIDN:AAK23480.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC1501
Query Match 1.7%; Score 7; DB 2; Length 240;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 136 FGDVGAL 142
| | | | |
Db 73 FGDVGAL 79

```

```

RESULT 35
H72691
probable hexulose-6-phosphate synthase APE0952 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: H72691
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72691
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-241 <RAW>
A;Cross-references: DDBJ:AF000060; NID:95104186; PIDN:BAA79936.1; PID:d1043722; PID:g510
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0952

Query Match 1.7%; Score 7; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 ALESRLG 147
DB 229 ALESRLG 235

RESULT 36
C82995
two-component response regulator OmpR PA5200 [imported] - Pseudomonas aeruginosa (strain
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C82995
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: C82995
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-247 <STO>
A;Cross-references: GB:AE004093; GB:AE004091; NID:g9951505; PIDN:AA08585.1; GSPDB:GN004
A;Experimental source: strain PA01
C;Genetics:
A;Gene: ompR; PA5200
C;Superfamily: ompR protein; response regulator homology

Query Match 1.7%; Score 7; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 LLSRELF 35
DB 49 LLSRELF 55

RESULT 37
E69455
conserved hypothetical protein AF1646 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: E69455
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

```

A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: E69455

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-261 <KLE>

A;Cross-references: GB:AE000989; GB:AE000782; NID:g2689312; PIDN:AA889596.1; PID:g264890

Query Match 1.7%; Score 7; DB 2; Length 261;

Best Local Similarity 100.0%; Pred. No. 87;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 KPTLENL 106

DB 187 KPTLENL 193

RESULT 38

T18886

hypothetical protein C03D6.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T18886

R;Burton, J.

submitted to the EMBL Data Library, June 1996

A;Reference number: Z19038

A;Accession: T18886

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-262 <WIL>

A;Cross-references: EMBL:Z75525; PIDN:CAA99766.1; GSPDB:GN00019; CESP:C03D6.1

A;Experimental source: clone C03D6

C;Genetics:

A;Gene: CESP:C03D6.1

A;Map position: 1

A;Introns: 21/2; 58/3; 125/3; 229/2

Query Match 1.7%; Score 7; DB 2; Length 262;

Best Local Similarity 100.0%; Pred. No. 87;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 FNGTSCP 273

DB 61 FNGTSCP 67

RESULT 39

T06613

hypothetical protein F16J13.130 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cross)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 22-Oct-1999

C;Accession: T06613

R;Revan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,

submitted to the Protein Sequence Database, April 1999

A;Reference number: Z15789

A;Accession: T06613

A;Molecule type: DNA

A;Residues: 1-267 <BEV>

A;Cross-references: EMBL:AL049638; GSPDB:GN00062; ATSP:F16J13.130

A;Experimental source: cultivar Columbia; BAC clone F16J13

C;Genetics:

A;Gene: ATSP:F16J13.130

A;Map position: 4

A;Introns: 80/2; 93/2; 130/1; 190/1; 228/2

Query Match 1.7%; Score 7; DB 2; Length 267;

Best Local Similarity 100.0%; Pred. No. 89;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 AISSLPT 337

DB 73 AISSLPT 79

```

RESULT 40
JQ0686
nosiheptide resistance protein - Streptomyces actuosus
C;Species: Streptomyces actuosus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 17-Mar-2000
C;Accession: JQ0686
R;Li, Y.; Dosch, D.C.; Strohl, W.R.; Floss, H.G.
Gene 91, 9-17, 1990
A;Title: Nucleotide sequence and transcriptional analysis of the nosiheptide-resistance
A;Reference number: JQ0685; MUID:90382703; PMID:2401410
A;Accession: JQ0686
A;Molecule type: DNA
A;Residues: 1-274 <LI>
A;Cross-references: GB:U75434; GB:M32744; NID:g1654409; PIDN:AAB17875.1; PID:g1654411
A;Experimental source: ATCC 25421
C;Genetics:
A;Gene: nsh
C;Superfamily: conserved hypothetical protein HI0860
C;Keywords: antibiotic resistance

Query Match      1.7%; Score 7; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 ADRRLR 10
      |||||
Db     156 ADRLLR 162

RESULT 41
T36288
probable ABC-type transport system ATP-binding chain - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: T36288
R;Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z21603
A;Accession: T36288
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-276 <SEE>
A;Cross-references: EMBL:AL049819; PIDN:CAB42665.1; GSPDB:GN000070; SCOEDB:SCF7.06C
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCF7.06C
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match      1.7%; Score 7; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy     177 LRRTGS 183
      |||||
Db     243 LRRTGS 249

RESULT 42
E87682
methyltransferase, UbiE/COQ5 family [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: E87682
R;Niernan, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.W.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87682
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-276 <STO>

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A;Cross-references: GB:AE005673; NID:g13425221; PIDN:AAK25457.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC3495

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```

Query Match      1.7%; Score 7; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy     215 ALLELAR 221
      |||||
Db     81 ALLELAR 87

```

RESULT 43

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B97536
ATP/GTP-binding protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: B97536
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goldman
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: B97536
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-285 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK87243.1; PID:g15156529; GSPDB:GN00169
C;Genetics:
A;Gene: AGR C 2676
A;Map position: circular chromosome

```

```

Query Match      1.7%; Score 7; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      3 EADRRLL 9
      |||||
Db     10 EADRRLL 16

```

RESULT 44

```

G71276
conserved hypothetical protein TP0829 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C;Accession: G71276
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi
rson, J.; Khaliq, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; MCD
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: G71276
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-294 <COL>
A;Cross-references: GB:AE001253; GB:AE000520; NID:g3323133; PIDN:AAC65795.1; PID:g33231
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0829

```

```

Query Match      1.7%; Score 7; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     216 LLELARQ 222
      |||||
Db     272 LLELARQ 278

```

RESULT 45

JC1120

sdsB protein - Pseudomonas sp.
C:Species: Pseudomonas sp.
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 24-Nov-1999
C:Accession: JC1120
R:Davidson, J.; Brunel, F.; Phanopoulos, A.; Prozzi, D.; Terpetra, P.
Gene 114, 19-24, 1992
A:Title: Cloning and sequencing of Pseudomonas genes determining sodium dodecyl sulfate
A:Reference number: JC1118; MUID:92267380; PMID:1587481
A:Accession: JC1120
A:Molecule type: DNA
A:Residues: 1-306 <DAV>
A:Cross-references: GB:M86744; NID:g151550; PIDN:AAA25988.1; PID:g151551
C:Genetics:
A:Gene: sdsB
C:Superfamily: conserved hypothetical protein HI1364

Query Match 1.7%; Score 7; DB 2; Length 306;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 LALLELA 220
|||
Db 256 LALLELA 262

RESULT 46

D75447
ABC transporter, ATP-binding protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: D75447
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: D75447
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-307 <WHI>
A:Cross-references: GB:AE001953; GB:AE000513; NID:g6458740; PIDN:AAF10588.1; PID:g645874
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1012
A:Map position: 1
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 1.7%; Score 7; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 VLALLEL 219
|||
Db 125 VLALLEL 131

RESULT 47

G64456
conserved hypothetical protein MJ1256 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: G64456
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
Reich, C.I.; Overberg, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: G64456
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-311 <BUL>
A:Cross-references: GB:U67566; GB:L77117; NID:g1591887; PIDN:AAB99260.1; PID:g1591890; T
C:Genetics:
A:Map position: FOR1198613-1199548
A:Start codon: GTG
C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ1256

Query Match 1.7%; Score 7; DB 1; Length 311;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 VSVKGIV 397
|||
Db 251 VSVKGIV 257

RESULT 48

S60713
polygalacturonase-inhibiting protein - soybean (fragment)
C:Species: Glycine max (soybean)
C>Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 17-Mar-1999
C:Accession: S60713
R:Favaron, F.; D'Ovidio, R.; Porceddu, E.; Alghisi, P.
Planta 195, 80-87, 1994
A:Title: Purification and molecular characterization of a soybean polygalacturonase-inhi
A:Reference number: S60713; MUID:95152348; PMID:7765794
A:Accession: S60713
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-313 <FAV>
A:Cross-references: EMBL:X78274; NID:g809547; PID:g809548
C:Superfamily: polygalacturonase-inhibiting protein; leucine-rich alpha-2-glycoprotein r

Query Match 1.7%; Score 7; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 PSLGGKP 279
|||
Db 191 PSLGGKP 197

RESULT 49

AB0350
probable membrane protein YPO2874 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AB0350
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AB0350
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-318 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC92125.1; PID:g15980841; GSPDB:GN00175
C:Genetics:
A:Gene: YPO2874

Query Match 1.7%; Score 7; DB 2; Length 318;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLRRCL 14
|||
Db 25 LLRRCL 31

RESULT 50

A72637
hypothetical protein APE1552 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: A72637
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; X
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: A72637
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-319 <KAW>
A:Cross-references: DBJ:AP000061; NID:G5104821; PIDN:BAA80551.1; PID:dl044337; PID:G510
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE1552

Query Match 1.7%; Score 7; DB 2; Length 319;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 46 AGSGSRR 52
|||||
DB 306 AGSGSRR 312

Search completed: August 3, 2004, 09:11:13
Job time : 21 secs